

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:15 ; Search time 42.75 seconds
(without alignments)
75.522 Million cell updates/sec

Title: US-10-032-950-1

Perfect score: 39

Sequence: 1 GVNAXSLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	97.4	9	3 AAY67860	Aay67860 Staphyloc
2	38	97.4	9	3 AAY67859	Aay67859 Staphyloc
3	38	97.4	9	5 ABB07160	Abb07160 Peptide-m
4	38	97.4	9	5 AAM50907	Aam50907 Protected
5	38	97.4	9	5 AAM51004	Aam51004 AgrD2 lac
6	38	97.4	9	5 AAM51003	Aam51003 AgrD2 lin
7	38	97.4	9	5 AAM51002	Aam51002 AgrD2 lin
8	37	94.9	9	3 AAY67851	Aay67851 S. aureus
9	37	94.9	9	3 AAY67861	Aay67861 Staphyloc
10	37	94.9	9	5 ABB07161	Abb07161 Peptide-m
11	37	94.9	9	5 AAM51005	Aam51005 AgrD2 lac
12	37	94.9	9	5 AAM50908	Aam50908 Protected
13	37	94.9	9	5 AAM50899	Aam50899 AgrD-auto
14	37	94.9	9	5 ABB53540	Abp53540 Cyclic pe
15	36	92.3	9	2 AAW38323	Aaw38323 Transcrip
16	36	92.3	9	5 ABB07159	Abb07159 Peptide-m
17	36	92.3	9	5 AAM51001	Aam51001 AgrD2 thi
18	36	92.3	9	6 ABB84631	Abb84631 S. aureus
19	36	92.3	9	7 ADF09190	Adf09190 S. aureus
20	36	92.3	9	8 ADJ98875	Adj98875 Peptide t
21	36	92.3	47	6 ABB84634	Abb84634 S. aureus
22	36	92.3	47	7 ADF09193	Adf09193 S. aureus
23	34	87.2	9	3 AAY67855	Aay67855 S. aureus
24	34	87.2	9	3 AAY67856	Aay67856 S. aureus
25	34	87.2	9	5 AAM50903	Aam50903 AgrD-auto

26	34	87.2	9	5 AAM50904	Aam50904 AgrD-auto
27	34	87.2	9	5 ABB53544	Abp53544 Cyclic pe
28	34	87.2	9	5 ABB53545	Abp53545 Cyclic pe
29	33	84.6	9	3 AAY67852	Aay67852 S. aureus
30	33	84.6	9	5 AAM50900	Aam50900 AgrD-auto
31	33	84.6	9	5 ABB53541	Abp53541 Cyclic pe
32	32	82.1	9	3 AAY67857	Aay67857 S. aureus
33	32	82.1	9	5 AAM50905	Aam50905 AgrD-auto
34	32	82.1	9	5 ABB53546	Abp53546 Cyclic pe
35	32	82.1	895	5 ABB92623	Abb92623 Herbicida
36	32	82.1	895	8 ADN72153	Adn72153 Thale cre
37	31	79.5	9	3 AAY67854	Aay67854 S. aureus
38	31	79.5	9	5 AAM50902	Aam50902 AgrD-auto
39	31	79.5	9	5 ABB53543	Abp53543 Cyclic pe
40	31	79.5	61	7 ADF04608	Adf04608 Bacterial
41	31	79.5	243	4 ARG13172	Arg13172 Novel hum
42	31	79.5	926	7 ADK62934	Adk62934 Disease t
43	30	76.9	447	7 ABO66851	Abo66851 Klebsiell
44	30	76.9	465	4 ABB63395	Abb63395 Drosophil
45	30	76.9	479	3 AAG29190	Aag29190 Arabidops

ALIGNMENTS

RESULT 1

AAY67860
ID AAY67860 standard; peptide; 9 AA.

XX

AC AAY67860;

XX

DT 25-APR-2000 (first entry)

XX

DE Staphylococcus aureus AgrDII derived peptide sequence.

XX

KW Staphylococcus aureus infection; AgrD; agr response; treatment;

KW virulence factor.

XX

OS Staphylococcus aureus.

XX

PN WO967286-A2.

XX

PD 29-DEC-1999.

XX

PF 24-JUN-1999; 99WO-US014562.

XX

PR 24-JUN-1998; 98US-00103438.

XX

PA (UYRQ) UNIV ROCKEFELLER.

XX

PI (UYNY) UNIV NEW YORK STATE.

XX

PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX

DR WPI; 2000-147202/13.

XX

XX New cyclic peptides for treating infections with Staphylococcus aureus.

XX

PS Example; Page 22; 37pp; English.

XX

XX This sequence represents the Staphylococcus aureus AgrDII derived

XX peptide. The invention relates to AgrD derived cyclic peptides, a

XX composition containing a peptide and a carrier, and a method for the

XX production of the cyclic peptides. The peptide inhibits the agr response,

XX which is normally associated with the release of virulence factors of

XX Staphylococcus aureus. An AgrD peptide is produced by S. aureus that

XX activates the agr response in strains of a single group, but interferes

XX with this response in strains of different groups. The peptides and

XX composition containing them can be used to treat infections by S. aureus

XX

SQ Sequence 9 AA;

Query Match 97.4%; Score 38; DB 3; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.7e+06;


```

FT      /note= "Ser(tBu)"
FT      6
FT      Modified-site
FT      /note= "Ser(Bzl)"
FT      7
FT      Modified-site
FT      /note= "Ser(Bzl)"
FT      8
FT      Misc-difference 9
FT      /note= "note linked to residue 5 to form cyclic peptide"
FT      9
FT      US6337385-B1.
FT      10
FT      08-JAN-2002.
FT      11
FT      24-JUN-1999; 99US-00339511.
FT      12
FT      24-JUN-1998; 98US-0090402P.
FT      13
FT      (UYRQ ) UNIV ROCKEFELLER.
FT      14
FT      (UYNY ) UNIV NEW YORK STATE.
FT      15
FT      Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
FT      16
FT      WPI; 2002-170774/22.
FT      17
FT      Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
FT      18
FT      interference and for treating Staphylococcus aureus infection in a
FT      19
FT      subject.
FT      20
FT      Disclosure; Col 14; 18pp; English.
FT      21
FT      The present sequence is that of a protected peptide used in an example of
FT      22
FT      the preparation of novel synthetic cyclic peptides of the invention (see
FT      23
FT      AAM5099-906). The peptide corresponds to the Staphylococcus aureus
FT      24
FT      AgrDII sequence with a Cys5 to Ser mutation (lactone). It was synthesised
FT      25
FT      on a Wang-resin using an Fmoc N-alpha protection strategy. Following
FT      26
FT      chain assembly, the peptide was cleaved from the support and the Ser-5
FT      27
FT      residue deprotected by treatment with a trifluoroacetic
FT      28
FT      acid:anisole:water mixture (90:5:5) for 4 hr. The partially protected
FT      29
FT      peptide-alpha carboxylates were then dissolved in DMF and treated with
FT      30
FT      PyBOP and a catalytic amount of dimethylaminopyridine. Cyclization was
FT      31
FT      complete after 2 hr. The remaining protecting groups were then removed by
FT      32
FT      treatment with HF and the peptide purified by HPLC. The cyclic peptide is
FT      33
FT      capable of inhibiting the agr response of Staphylococcus aureus. The
FT      34
FT      thiolactone structure within native AgrD peptides is required for
FT      35
FT      activation of this response. Replacement of the thiol ester component of
FT      36
FT      the cyclic ring structure with a lactone (as in the present case) or a
FT      37
FT      lactam can destroy agr response activating activity while preserving and
FT      38
FT      enhancing inhibitory activity. The cyclic peptides are useful for
FT      39
FT      bacterial interference, especially for the treatment of S. aureus
FT      40
FT      infection
FT      41
FT      SQ      Sequence 9 AA;
FT      42
FT      Query Match      97.4%; Score 38; DB 5; Length 9;
FT      43
FT      Best Local Similarity 88.9%; Pred. No. 1.7e+06;
FT      44
FT      Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
FT      45
FT      QY      1 GVNAXSSLF 9
FT      46
FT      DB      1 GVNAXSSLF 9
FT      47
FT      RESULT 5
FT      48
FT      AAM51004
FT      49
FT      ID      AAM51004 standard; peptide; 9 AA.
FT      50
FT      XX
FT      51
FT      AC      AAM51004;
FT      52
FT      XX
FT      53
FT      DT      07-AUG-2003 (revised)
FT      54
FT      DT      08-MAY-2002 (first entry)
FT      55
FT      XX
FT      56
FT      DE      AgrD2 lactone cyclic peptide.
FT      57
FT      XX
FT      58
FT      KW      AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
FT      59
FT      therapy; lactone; cyclic.
FT      60
FT      OS      Staphylococcus aureus.
FT      61
FT      OS      Synthetic.
FT      62
FT      XX
FT      63
FT      FH      Key      Location/Qualifiers
FT      64
FT      FT      Misc-difference 5;
FT      65
FT      FT      /note= "note linked to residue 9 to form cyclic peptide"
FT      66
FT      FT      Misc-difference 9;
FT      67
FT      FT      /note= "note linked to residue 5 to form cyclic peptide"
FT      68
FT      XX
FT      69
FT      PN      US6337385-B1.
FT      70
FT      XX
FT      71
FT      PD      08-JAN-2002.
FT      72
FT      XX
FT      73
FT      PF      24-JUN-1999; 99US-00339511.
FT      74
FT      XX
FT      75
FT      PR      24-JUN-1998; 98US-0090402P.
FT      76
FT      XX
FT      77
FT      PA      (UYRQ ) UNIV ROCKEFELLER.
FT      78
FT      PA      (UYNY ) UNIV NEW YORK STATE.
FT      79
FT      XX
FT      80
FT      PI      Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
FT      81
FT      XX
FT      82
FT      DR      WPI; 2002-170774/22.
FT      83
FT      XX
FT      84
FT      PT      Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
FT      85
FT      PT      interference and for treating Staphylococcus aureus infection in a
FT      86
FT      PT      subject.
FT      87
FT      PS      Example 1; Col 9; 18pp; English.
FT      88
FT      XX
FT      89
FT      CC      The present sequence is that of a novel synthetic AgrD2 lactone cyclic
FT      90
FT      CC      peptide in which residue 5 of the peptide is linked to residue 9 via a
FT      91
FT      CC      lactone bond. The peptide is derived from an AgrD2 peptide of
FT      92
FT      CC      Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
FT      93
FT      CC      where the agr locus controls the synthesis of virulence factor and other
FT      94
FT      CC      extracellular proteins responsible for pathogenicity in S. aureus. The
FT      95
FT      CC      biological activity of the synthetic peptide was assayed using cultured
FT      96
FT      CC      S. aureus strains containing a beta-lactamase reporter gene fused to the
FT      97
FT      CC      agrP3 promoter. This allowed activation or inhibition of the agr response
FT      98
FT      CC      to be monitored spectrophotometrically. The lactone AgrD2 peptide
FT      99
FT      CC      inhibited the agr response of group I S. aureus strains without
FT      100
FT      CC      activating the agr response in group I, II or III strains. The invention
FT      101
FT      CC      provides claimed cyclic peptides (see AAM5099-906 and AAM50399) and
FT      102
FT      CC      methods for preparing them, especially peptides where the cyclic bond is
FT      103
FT      CC      a lactam or lactone bond. The cyclic peptides are useful for bacterial
FT      104
FT      CC      interference, especially for the treatment of S. aureus infection.
FT      105
FT      CC      (Updated on 07-AUG-2003 to correct OS field.)
FT      106
FT      XX
FT      107
FT      SQ      Sequence 9 AA;
FT      108
FT      Query Match      97.4%; Score 38; DB 5; Length 9;
FT      109
FT      Best Local Similarity 88.9%; Pred. No. 1.7e+06;
FT      110
FT      Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
FT      111
FT      QY      1 GVNAXSSLF 9
FT      112
FT      DB      1 GVNAXSSLF 9
FT      113
FT      RESULT 6
FT      114
FT      AAM51003
FT      115
FT      ID      AAM51003 standard; peptide; 9 AA.
FT      116
FT      XX
FT      117
FT      AC      AAM51003;
FT      118
FT      XX
FT      119
FT      DT      08-MAY-2002 (first entry)
FT      120
FT      XX
FT      121
FT      DE      AgrD2 linear free acid peptide.
FT      122
FT      XX
FT      123
FT      KW      AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
FT      124
FT      KW      therapy.

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XX OS Staphylococcus aureus.
XX OS Synthetic.
XX PN US6337385-B1.
XX PD 08-JAN-2002.
XX XX 24-JUN-1999; 99US-00339511.
XX PR 24-JUN-1998; 98US-0090402P.
XX XX (UYRQ ) UNIV ROCKEFELLER.
XX PA (UYNV ) UNIV NEW YORK STATE.
XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX DR WPI; 2002-170774/22.
XX PT Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
XX PT interference and for treating Staphylococcus aureus infection in a
XX PT subject.
XX PS Example 1; Col 9; 18pp; English.
XX CC The present sequence is that of a novel synthetic AgrD2 linear free acid
XX CC peptide. The peptide is derived from the cyclic AgrD2 peptide of
XX CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
XX CC where the agr locus controls the synthesis of virulence factor and other
XX CC extracellular proteins responsible for pathogenicity in S. aureus. The
XX CC biological activity of the synthetic peptide was assayed using cultured
XX CC S. aureus strains containing a beta-lactamase reporter gene fused to the
XX CC agrP3 promoter. This allowed activation or inhibition of the agr response
XX CC at uM concentrations. The invention provides claimed cyclic peptides (see
XX CC cyclic peptide (see AAM51001), the present peptide was unable to either
XX CC activate or inhibit the agr response, even when added to cultured cells
XX CC at uM concentrations. The invention provides claimed cyclic peptides (see
XX CC AAM50899-906 and AAM50999) and methods for preparing them. The cyclic
XX CC peptides are useful for bacterial interference, especially for the
XX CC treatment of S. aureus infection
XX SQ Sequence 9 AA;

Query Match 97.4%; Score 38; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSLF 9
Db |||||
1 GVNASSSLF 9

RESULT 7
AAM51002
ID AAM51002 standard; peptide; 9 AA.
XX AC AAM51002;
XX AC AAM51002;
XX DT 08-MAY-2002 (first entry)
XX DE AgrD2 linear thioester peptide.
XX KW AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
XX KW therapy.
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Modified-site 9 /note= "C-terminal thioester"
XX XX US6337385-B1.

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XX OS 08-JAN-2002.
XX PD 24-JUN-1999; 99US-00339511.
XX PF 24-JUN-1998; 98US-0090402P.
XX PR (UYRQ ) UNIV ROCKEFELLER.
XX PA (UYNV ) UNIV NEW YORK STATE.
XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX DR WPI; 2002-170774/22.
XX PT Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
XX PT interference and for treating Staphylococcus aureus infection in a
XX PT subject.
XX PS Example 1; Col 9; 18pp; English.
XX CC The present sequence is that of a novel synthetic AgrD2 linear thioester
XX CC peptide. The peptide is derived from the cyclic AgrD2 peptide of
XX CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
XX CC where the agr locus controls the synthesis of virulence factor and other
XX CC extracellular proteins responsible for pathogenicity in S. aureus. The
XX CC biological activity of the synthetic peptide was assayed using cultured
XX CC S. aureus strains containing a beta-lactamase reporter gene fused to the
XX CC agrP3 promoter. This allowed activation or inhibition of the agr response
XX CC to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone
XX CC cyclic peptide (see AAM51001), the present peptide was unable to either
XX CC activate or inhibit the agr response, even when added to cultured cells
XX CC at uM concentrations. The invention provides claimed cyclic peptides (see
XX CC AAM50899-906 and AAM50999) and methods for preparing them. The cyclic
XX CC peptides are useful for bacterial interference, especially for the
XX CC treatment of S. aureus infection
XX SQ Sequence 9 AA;

Query Match 97.4%; Score 38; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSLF 9
Db |||||
1 GVNASSSLF 9

RESULT 8
AAY67851
ID AAY67851 standard; peptide; 9 AA.
XX AC AAY67851;
XX AC AAY67851;
XX DT 25-APR-2000 (first entry)
XX DE S. aureus peptide #1 used for bacterial interference.
XX KW Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;
XX KW virulence factor; treatment.
XX OS Staphylococcus aureus.
XX PH Key Location/Qualifiers
XX FT Misc-difference 5 /label= Unknown
XX FT WO9967286-A2.
XX PN 29-DEC-1999.
XX PD 24-JUN-1999; 99WO-US014562.
XX PF 24-JUN-1998; 98US-00103438
XX PR 24-JUN-1998; 98US-00103438

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CC quorum sensing
XX Sequence 9 AA;
SQ
  Query Match          94.9%; Score 37; DB 5; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.7e+06;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVNAXSSLF 9
Db 1 GVNAXSSLF 9

RESULT 11
AAM51005
ID AAM51005 standard; peptide; 9 AA.
XX
AC AAM51005;
XX
DT 07-AUG-2003 (revised)
DT 08-MAY-2002 (first entry)
XX
DE AgrD2 lactam cyclic peptide.
XX
KW AgrD2; agr response; inhibitor; antibacterial; infection;
KW therapy; cyclic.
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"
FT Misc-difference 5 /note= "any amino acid"
FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"
XX
FN US6337385-B1.
XX
PD 08-JAN-2002.
XX
PF 24-JUN-1999; 99US-00339511.
XX
PR 24-JUN-1998; 98US-0090402P.
XX
PA (UVRQ ) UNIV ROCKEFELLER.
PA (UVRQ ) UNIV NEW YORK STATE.
XX
PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX
DR WPI; 2002-170774/22.
XX
Novel synthetic, cyclic AgrD2-autoinducing peptide for bacterial
interference and for treating Staphylococcus aureus infection in a
subject.
XX
Example 1; Col 11; 18pp; English.
XX
The present sequence is that of a novel synthetic AgrD2 lactam cyclic
peptide in which residue 5 of the peptide is linked to residue 9 via a
lactam bond. The peptide is derived from an AgrD2 peptide of
Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
where the agr locus controls the synthesis of virulence factor and other
extracellular proteins responsible for pathogenicity in S. aureus. The
biological activity of the synthetic peptide was assayed using cultured
S. aureus strains containing a beta-lactamase reporter gene fused to the
agrP3 promoter. This allowed activation or inhibition of the agr response
to be monitored spectrophotometrically. The AgrD3 lactam peptide
inhibited the agr response in group I S. aureus strains and did not
activate the agr response in group II, III or IV strains. The invention
provides claimed cyclic peptides (see AAM50899-906 and AAM50999) and
methods for preparing them, especially where the cyclic bond is a lactam

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CC or lactone bond. The cyclic peptides are useful for bacterial
CC interference, especially for the treatment of S. aureus infection.
CC (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 9 AA;
  Query Match          94.9%; Score 37; DB 5; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.7e+06;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVNAXSSLF 9
Db 1 GVNAXSSLF 9

RESULT 12
AAM50908
ID AAM50908 standard; peptide; 9 AA.
XX
AC AAM50908;
XX
DT 08-MAY-2002 (first entry)
XX
DE Protected peptide used in cyclic peptide production.
XX
KW Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
KW antibacterial; infection; therapy; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Z-Gly"
FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"
FT Modified-site 5 /note= "label= Dpr(Boc)"
FT Modified-site 6 /note= "Ser(Bzl)"
FT Modified-site 7 /note= "Ser(Bzl)"
FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"
XX
FN US6337385-B1.
XX
PD 08-JAN-2002.
XX
PF 24-JUN-1999; 99US-00339511.
XX
PR 24-JUN-1998; 98US-0090402P.
XX
PA (UVRQ ) UNIV ROCKEFELLER.
PA (UVRQ ) UNIV NEW YORK STATE.
XX
PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX
DR WPI; 2002-170774/22.
XX
Novel synthetic, cyclic AgrD2-autoinducing peptide for bacterial
interference and for treating Staphylococcus aureus infection in a
subject.
XX
Disclosure; Col 14; 18pp; English.
XX
The present sequence is that of a protected peptide used in an example of
the preparation of novel synthetic cyclic peptides of the invention (see
AAM50899-906). The peptide corresponds to the Staphylococcus aureus
AgrDII sequence with a Cys5 to diaminopropionic acid (Dpr) mutation
(lactam). It was synthesized on a Wang-resin using an Fmoc N-alpha
protection strategy. Following chain assembly, the peptide was cleaved
from the support and the Dpr-5 residue deprotected by treatment with a
trifluoroacetic acid:anisole:water mixture (90:5:5) for 4 hr. The

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CC partially protected peptide-alpha carboxylates were then dissolved in DMF
 CC and treated with PyBOP. Cyclization was complete after 2 hr. The
 CC remaining protecting groups were removed by treatment with HF and the
 CC peptide purified by HPLC. The cyclic peptide is capable of inhibiting the
 CC agr response of *Staphylococcus aureus*. The thiololactone structure within
 CC native AgrD peptides is required for activation of this response.
 CC Replacement of the thiol ester component of the cyclic ring structure
 CC with a lactam (as in the present case) or a lactone can destroy agr
 CC response activating activity while preserving and enhancing inhibitory
 CC activity. The cyclic peptides are useful for bacterial interference,
 CC especially for the treatment of *S. aureus* infection

XX Sequence 9 AA;

Query Match 94.9%; Score 37; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXSSLF 9
 |||||
 DB 1 GVNAXSSLF 9

RESULT 13
 AAM50899
 ID AAM50899 standard; peptide; 9 AA.

AC AAM50899;

DT 08-MAY-2002 (first entry)

DE AgrD-autoinducing cyclic peptide, inhibitor of agr response.

KW *Staphylococcus aureus*; AgrD; agr response; inhibitor; antibiotic;

KW antibacterial; infection; therapy; cyclic.

XX Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"

FT Misc-difference 5 /note= "any amino acid"

FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"

XX US6337385-B1.

PN 08-JAN-2002.

PD 24-JUN-1999; 98US-00339511.

PF 24-JUN-1999; 98US-0090402P.

PR (UYRQ) UNIV ROCKEFELLER.

PA (UYNV) UNIV NEW YORK STATE.

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX WPI; 2002-170774/22.

XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 PT interference and for treating *Staphylococcus aureus* infection in a
 PT subject.

PS Claim 7; Col 19; 18pp; English.

XX The present sequence is that of a novel synthetic cyclic peptide of the
 CC invention that is capable of inhibiting the agr response of
 CC *Staphylococcus aureus*. It is an AgrD-autoinducing peptide, where AgrD is
 CC a secreted agr-encoded peptide and where the agr locus controls the
 CC synthesis of virulence factor and other extracellular proteins
 CC responsible for pathogenicity in *S. aureus*. Preferred peptides may have

CC the sequence NH₂-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z
 CC residue and COOH other than a thioester bond, where X is an amino acid,
 CC an amino acid analogue, a peptidomimetic or non-amide isostere. Z is a
 CC synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The
 CC cyclic bond is especially a lactam or lactone bond. The thiololactone
 CC structure within native AgrD peptides is required for activation of the
 CC agr response. Elimination of the thiol ester component of the cyclic ring
 CC structure can destroy agr response activating activity while preserving
 CC and enhancing inhibitory activity. A claimed method of preparing a cyclic
 CC peptide involves: assembling a linear peptide chain on to a solid phase
 CC resin support; deprotecting the resulting protected assembled peptide;
 CC treating the deprotected peptide with neutral buffer for a time
 CC sufficient to form the cyclic peptide and cleave the peptide from the
 CC support; and recovering the cyclic peptide. The peptide is useful for
 CC bacterial interference, especially for the treatment of *S. aureus*
 CC infection

XX Sequence 9 AA;

Query Match 94.9%; Score 37; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXSSLF 9
 |||||
 DB 1 GVNAXSSLF 9

RESULT 14

ABP53540
 ID ABP53540 standard; peptide; 9 AA.

XX ABP53540;

XX 13-DEC-2002 (first entry)

DE Cyclic peptide SEQ ID NO:1.

XX Cyclic peptide; *Staphylococcus aureus*; infection; antibacterial;
 KW agr response inhibitor.

XX Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 5 /note= "any amino acid"

XX US2002077453-A1.

PN 20-JUN-2002.

PD 27-DEC-2001; 2001US-00032950.

PF 24-JUN-1998; 98US-0090402P.

PR 24-JUN-1999; 99US-00339511.

XX (MUIR/) MUIR T W.

XX (MAYV/) MAYVILLE P.

XX (NOVI/) NOVICK R P.

XX (BEAV/) BEAVIS R.

XX (JIGG/) JI G.

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX WPI; 2002-681366/73.

XX New cyclic peptides, useful for treating *Staphylococcus aureus*
 PT infections.

PS Claim 9; Page 10; 18pp; English.

XX ABP53540 to ABP53547 represent cyclic peptides (I) from the present
 CC invention. The present invention also describes a method for treating

CC Staphylococcus aureus infection comprising the administration of a
 CC composition comprising (I). (I) has antibacterial activity, and can be
 CC used as an agr gene response inhibitor. The peptides are useful for
 CC treating S. aureus infections

XX SQ Sequence 9 AA;

Query Match 94.9%; Score 37; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9

RESULT 15

AAW38323
 ID AAW38323 standard; peptide; 9 AA.

XX AC AAW38323;

XX DT 28-MAY-1998 (first entry)

XX DE Transcription inhibitory peptide 3.

XX KW Transcription inhibitory peptide; inhibition; antibiotic; abscesses;
 XX KW endocarditis; pneumonia; osteomyelitis; virulence factor; agr regulator;
 XX KW agr-rnaii gene; colonisation.

XX OS Synthetic.

XX OS Staphylococcus aureus.

FH Key Location/Qualifiers

FT Misc-difference 5 /note= "linked to the carboxy terminus via a cyclic
 FT thioester bond"

XX PN W09744349-A1.

XX PD 27-NOV-1997.

XX PF 22-MAY-1997; 9TWO-US008791.

XX PR 22-MAY-1996; 96US-00651226.

XX PA (UWNY) UNIV NEW YORK STATE.

XX PI Novick RP, Beavis R;

XX PS WPI; 1998-018426/02.

FT Peptide inhibiting agr-rnaii transcription in Staphylococcus aureus -
 FT useful to treat S. aureus infection.

XX PS Claim 7; Page 15; 24pp; English.

XX CC This novel peptide sequence (or it's analogue) inhibits agr-rnaii
 CC transcription in Staphylococcus aureus (S. aureus), and is 9 amino acids
 CC long. The peptide can be added to pharmaceutical compositions to treat or
 CC prevent infections or diseases caused by S. aureus in animals, and
 CC especially in humans. They can also be combined with traditional
 CC antibiotics. S. aureus causes conditions ranging from abscesses (boils
 CC and furuncles) to life-threatening infections e.g. endocarditis,
 CC pneumonia, osteomyelitis, by secreting injurious proteins, or virulence
 CC factors. The synthesis of virulence factors is controlled by the agr
 CC regulator, which activates transcription of the agr-rnaii gene to
 CC produce RNAIII, which induces transcription of the genes encoding the
 CC virulence factors. The peptides inhibit agr-rnaii transcription in and
 CC therefor virulence factor expression. The peptides can also be used in
 CC vitro to prevent Staphylococcus aureus colonisation

XX SQ Sequence 9 AA;

Query Match 92.3%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9

Search completed: October 26, 2004, 15:59:38
 Job time : 43.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:54:00 ; Search time 31.5 Seconds
(without alignments)
92.502 Million cell updates/sec

Title: US-10-032-950-1

Perfect score: 39
Sequence: 1 GVNAAXSLF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	94.9	9	13 US-10-032-950-1	Sequence 1, Appli
2	36	92.3	9	14 US-10-201-444-3	Sequence 3, Appli
3	36	92.3	47	14 US-10-201-444-6	Sequence 6, Appli
4	34	87.2	9	13 US-10-032-950-5	Sequence 5, Appli
5	34	87.2	9	13 US-10-032-950-6	Sequence 6, Appli
6	33	84.6	9	13 US-10-032-950-2	Sequence 2, Appli
7	32	82.1	9	13 US-10-032-950-7	Sequence 7, Appli
8	31	79.5	9	13 US-10-032-950-4	Sequence 4, Appli
9	31	79.5	313	16 US-10-437-963-189388	Sequence 189388,
10	30	76.9	465	13 US-10-108-605-227	Sequence 227, App
11	30	76.9	465	14 US-10-004-378A-130	Sequence 130, App
12	30	76.9	465	14 US-10-004-378A-131	Sequence 131, App
13	30	76.9	633	14 US-10-369-493-6225	Sequence 6225, Ap

Sequence 3, Appli
Sequence 242903,
Sequence 260806,
Sequence 276931,
Sequence 205071,
Sequence 171012,
Sequence 72245, A
Sequence 40431, A
Sequence 1603, App
Sequence 48025, A
Sequence 46, Appli
Sequence 10385, A
Sequence 56166, A
Sequence 56741, A
Sequence 60169, A
Sequence 73336, A
Sequence 73407, A
Sequence 58, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 168044,
Sequence 110, App
Sequence 78248, A
Sequence 168045,
Sequence 459, App
Sequence 9, Appli
Sequence 459, App
Sequence 459, App

9 13 US-10-032-950-3
55 15 US-10-424-599-242903
60 15 US-10-424-599-260806
81 15 US-10-424-599-276931
93 15 US-10-424-599-205071
167 15 US-10-424-599-171012
271 15 US-10-282-122A-72245
294 16 US-10-767-701-40441
311 16 US-10-408-765A-1603
317 15 US-10-282-122A-48025
332 14 US-10-145-586-46
382 9 US-09-815-242-10385
382 15 US-10-282-122A-56166
382 15 US-10-282-122A-56741
382 15 US-10-282-122A-60169
382 15 US-10-282-122A-73336
411 16 US-10-282-122A-75407
416 14 US-10-451-793-58
416 14 US-10-371-525-26
416 14 US-10-371-069-26
416 14 US-10-371-645-26
490 14 US-10-371-260-26
490 14 US-10-243-351-3
589 16 US-10-437-963-168044
605 15 US-10-100-303A-110
618 15 US-10-282-122A-78248
653 16 US-10-437-963-168045
747 9 US-09-978-295A-459
747 9 US-09-938-418-9
747 9 US-09-978-697-459
747 9 US-09-978-192A-459

ALIGNMENTS

RESULT 1
US-10-032-950-1
; Sequence 1. Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-1

Query Match 94.9%; Score 37; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVNAAXSLF 9

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Db      1  GVNAXSSLF 9
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RESULT 2
US-10-201-444-3
; Sequence 3, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; CURRENT APPLICATION NUMBER: US/10/201,444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-3
Query Match      92.3%; Score 36; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GVNAXSSLF 9
      |||||
Db      1  GVNACSSLF 9

RESULT 3
US-10-201-444-6
; Sequence 6, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT APPLICATION NUMBER: US/10/201,444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-6
Query Match      92.3%; Score 36; DB 14; Length 47;
Best Local Similarity 88.9%; Pred. No. 0.87;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GVNAXSSLF 9
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Db      24  GVNACSSLF 32

RESULT 4
US-10-032-950-5
; Sequence 5, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-6
Query Match      87.2%; Score 34; DB 13; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  GVNAXSSLF 9
      |||||
Db      1  GVNAXSALF 9

RESULT 5
US-10-032-950-6
; Sequence 6, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-6
Query Match      87.2%; Score 34; DB 13; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  GVNAXSSLF 9
      |||||
Db      1  GVNAXSALF 9

RESULT 6
US-10-032-950-2
; Sequence 2, Application US/10032950
; Publication No. US20020077453A1

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; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-2

Query Match      84.6%; Score 33; DB 13; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSSLF 9
| | | | |
Db 1 GANAXSSLF 9

RESULT 7
US-10-032-950-7
; Sequence 7, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-7

Query Match      82.1%; Score 32; DB 13; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSSLF 9
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Db 1 GVNAXSSAF 9

RESULT 8
US-10-032-950-4
; Sequence 4, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
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; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-4

Query Match      79.5%; Score 31; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNXSSSLF 9
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Db 2 VNXSSSLF 9

RESULT 9
US-10-437-963-189388
; Sequence 189388, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189388
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) .. (313)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MET4530_85902C.1.pap
US-10-437-963-189388

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Query Match 79.5%; Score 31; DB 16; Length 313;
 Best Local Similarity 55.6%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNXSSLF 9
 | : | | : |
 Db 102 GINGTSSIF 110

RESULT 10

US-10-108-605-227
 ; Sequence 227, Application US/10108605
 ; Publication No. US20020160934A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Broadus, Julie
 ; APPLICANT: Stam, Lynn
 ; APPLICANT: Bachmann, Jane
 ; APPLICANT: Kandari, Kim
 ; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
 ; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
 ; FILE REFERENCE: 31133B
 ; CURRENT APPLICATION NUMBER: US/10/108,605
 ; CURRENT FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: US 03/761,142
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/176,418
 ; PRIOR FILING DATE: 2000-01-14
 ; NUMBER OF SEQ ID NOS: 361
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 227
 ; LENGTH: 465
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-10-108-605-227

Query Match 76.9%; Score 30; DB 13; Length 465;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNXSSLF 9
 | : | | : |
 Db 339 GVNLFSSIF 347

RESULT 11

US-10-004-378A-130
 ; Sequence 130, Application US/10004378A
 ; Publication No. US20030228301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Li
 ; APPLICANT: Furtak, Kazarzyna
 ; APPLICANT: Perna, Amanda
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Guo, Xiaojia Sasha
 ; APPLICANT: Casman, Stacie J
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Malyankar, Uriel M
 ; APPLICANT: Tchernev, Velizar T
 ; APPLICANT: Vernet, Corrine A
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Agee, Michele
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Shenoy, Suresh G
 ; APPLICANT: Grosse, William M
 ; APPLICANT: Alsobrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Edinger, Schlomit
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Peyman, John A
 ; APPLICANT: Gunther, Erik

; APPLICANT: Stone, David J
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Gangolli, Esha A
 ; TITLE OF INVENTION: No. US20030228301A1 Human Proteins, Polynucleotides Encoding Th
 ; FILE REFERENCE: 21402-179
 ; CURRENT APPLICATION NUMBER: US/10/004,378A
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,882
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,765
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/300,206
 ; PRIOR FILING DATE: 2001-06-22
 ; PRIOR APPLICATION NUMBER: 60/242,789
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,768
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,767
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/243,622
 ; PRIOR FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: 60/273,047
 ; PRIOR FILING DATE: 2001-03-02
 ; PRIOR APPLICATION NUMBER: 60/243,591
 ; PRIOR FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: 60/243,950
 ; PRIOR FILING DATE: 2000-10-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 191
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 130
 ; LENGTH: 465
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-10-004-378A-130

Query Match 76.9%; Score 30; DB 14; Length 465;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNXSSLF 9
 | : | | : |
 Db 339 GVNLFSSIF 347

RESULT 12

US-10-004-378A-131
 ; Sequence 131, Application US/10004378A
 ; Publication No. US20030228301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Li
 ; APPLICANT: Furtak, Kazarzyna
 ; APPLICANT: Perna, Amanda
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Guo, Xiaojia Sasha
 ; APPLICANT: Casman, Stacie J
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Malyankar, Uriel M
 ; APPLICANT: Tchernev, Velizar T
 ; APPLICANT: Vernet, Corrine A
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Agee, Michele
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Shenoy, Suresh G
 ; APPLICANT: Grosse, William M
 ; APPLICANT: Alsobrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Edinger, Schlomit
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Peyman, John A

; APPLICANT: Gunther, Erik
 ; APPLICANT: Stone, David J
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Gangolli, Esha A
 ; TITLE OF INVENTION: No. US20030228301A1el Human Proteins, Polynucleotides Encoding Th
 ; TITLE OF INVENTION: Methods of Using the Same
 ; FILE REFERENCE: 21402-179
 ; CURRENT APPLICATION NUMBER: US/10/004,378A
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,882
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,765
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/300,206
 ; PRIOR FILING DATE: 2001-06-22
 ; PRIOR APPLICATION NUMBER: 60/242,789
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,768
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,767
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/243,622
 ; PRIOR FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: 60/273,047
 ; PRIOR FILING DATE: 2001-03-02
 ; PRIOR APPLICATION NUMBER: 60/243,591
 ; PRIOR FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: 60/243,950
 ; PRIOR FILING DATE: 2000-10-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 191
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 131
 ; LENGTH: 465
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-10-004-378A-131

Query Match 76.9%; Score 30; DB 14; Length 465;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSLF 9
 ||| |||
 DB 339 GVNLFSSIF 347

RESULT 13
 US-10-369-493-6225
 ; Sequence 6225, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Harry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 6225
 ; LENGTH: 633
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-369-493-6225

Query Match 76.9%; Score 30; DB 14; Length 633;
 Best Local Similarity 75.0%; Pred. No. 3.7e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 VNXAXSSLF 9
 :||| |||
 DB 328 INAFSSLF 335

RESULT 14
 US-10-032-950-3
 ; Sequence 3, Application US/10032950
 ; Publication No. US20020077453A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Muir, Tom
 ; APPLICANT: Mayville, Patricia
 ; APPLICANT: No. US20020077453A1lick, Richard P.
 ; APPLICANT: Beavis, Ronald
 ; APPLICANT: Ji, Guangyong
 ; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
 ; TITLE OF INVENTION: INTERFERENCE
 ; FILE REFERENCE: 600-1-231N
 ; CURRENT APPLICATION NUMBER: US/10/032,950
 ; CURRENT FILING DATE: 2001-12-27
 ; PRIOR APPLICATION NUMBER: 60/090,402
 ; PRIOR FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 ; NAME/KEY: VARIANT
 ; LOCATION: (5)
 ; OTHER INFORMATION: Xaa represents any amino acid at this position.
 US-10-032-950-3

Query Match 74.4%; Score 29; DB 13; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSLF 9
 ||| |||
 DB 1 GVAAXSSLF 9

RESULT 15
 US-10-424-599-242903
 ; Sequence 242903, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 242903
 ; LENGTH: 55
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_61370C.1.pap
 US-10-424-599-242903

Query Match 74.4%; Score 29; DB 15; Length 55;
 Best Local Similarity 66.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSLF 9
Db 23 GVEATSLF 31

Search completed: October 26, 2004, 16:10:09
Job time : 32.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:46:55 ; Search time 8.73529 Seconds
(without alignments)
99.132 Million cell updates/sec

Title: US-10-032-950-1

Perfect score: 39

Sequence: 1 GVNAXSSLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	92.3	47	2 C89995	AgrD protein [impo
2	35	89.7	382	2 A28067	lysosomal membrane
3	35	89.7	405	2 A60534	P2B/LAMP-1 precurs
4	35	89.7	407	2 A30200	120K lysosomal mem
5	34	87.2	333	1 C69812	ferrichrome ABC tr
6	32	82.1	895	2 T45786	receptor-protein k
7	31	79.5	389	1 S36653	kpsD protein - Esc
8	31	79.5	394	2 B81286	probable polysacch
9	31	79.5	631	2 D89750	phosphotransferase
10	31	79.5	926	2 S48463	SEC24 protein - ye
11	30	76.9	109	2 A99227	hypothetical prote
12	30	76.9	420	2 AD0105	probable sugar-bin
13	30	76.9	560	2 T02404	probable beta-gluc
14	30	76.9	633	2 T27215	hypothetical prote
15	29	74.4	269	2 S58439	transcription fact
16	29	74.4	369	2 B43715	protein M homolog
17	29	74.4	382	2 AH0976	mannitol-1-phospha
18	29	74.4	382	2 B65160	mannitol-1-phospha
19	29	74.4	398	2 F85056	hypothetical prote
20	29	74.4	416	1 A31959	lysosome-associated
21	29	74.4	453	1 ZBQC02	ubiquinol-cytochro
22	29	74.4	500	1 E8FF	zip protein precur
23	29	74.4	618	2 AB0186	probable exported
24	29	74.4	655	2 G89189	protein Y32F6A.3 [
25	29	74.4	746	2 T01536	hypothetical prote
26	29	74.4	963	2 T26022	hypothetical prote
27	29	74.4	1054	2 A30239	hydroxymethylgluta
28	29	74.4	1435	2 T32930	hypothetical prote
29	28	71.8	53	2 AF2557	hypothetical prote

30	28	71.8	271	2 F90350	hypothetical prote
31	28	71.8	346	2 S85491	probable galactosy
32	28	71.8	349	2 S74439	iron(III) dicitrat
33	28	71.8	350	2 E64499	hypothetical prote
34	28	71.8	381	1 A53224	ubiquinol-cytochro
35	28	71.8	381	2 S12023	ubiquinol-cytochro
36	28	71.8	421	2 C70038	maltose/maltodextr
37	28	71.8	424	2 C83902	maltose/maltodextr
38	28	71.8	442	2 AF2539	manganese transpor
39	28	71.8	468	2 T24523	hypothetical prote
40	28	71.8	476	2 D86306	Similar to Cytochr
41	28	71.8	480	2 C96744	hypothetical prote
42	28	71.8	514	2 T47837	beta-glucosidase-1
43	28	71.8	549	2 F64640	conserved hypother
44	28	71.8	558	2 F82236	peptidase (M3 fami
45	28	71.8	573	2 F81313	

ALIGNMENTS

RESULT 1

C89995

AgrD protein [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: C89995

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: C89995

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-47 <XUR>

A:Cross-references: UNIPROT:O33586; GB:BA000018; PID:gl3701831; PIDN:BA843124.1; GSPDB:

A:Experimental source: strain N315

C:Genetics:

A:Gene: agrD

Query Match 92.3%; Score 36; DB 2; Length 47;
Best Local Similarity 88.9%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSLF 9
||| ||||
Db 24 GVNACSSLF 32

RESULT 2

A28067

lysosomal membrane glycoprotein LAMP-1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C:Accession: A28067

R:Chen, J.W.; Cha, Y.; Yuxsel, K.U.; Gracy, R.W.; August, J.T.

J. Biol. Chem. 263, 8754-8758, 1988

A:Title: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprot

A:Reference number: A28067; MUID:88243732; PMID:3373044

A:Accession: A28067

A:Molecule type: mRNA

A:Residues: 1-382 <CHE>

A:Cross-references: UNIPROT:P11438; GB:J03881; NID:gl98706; PIDN:AAA39411.1; PID:g29369

A:Note: the authors translated the codon ATT for residue 1 as Leu and CCG for residue 2

C:Superfamily: lysosome-associated membrane protein

C:Keywords: glycoprotein; membrane protein

Query Match 89.7%; Score 35; DB 2; Length 382;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

C;Accession: S36653; E48492; C42644
R;Roberts, I.S.
Submitted to the EMBL Data Library, August 1993
A;Reference number: S36649
A;Accession: S36653
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <ROB>
A;Cross-references: UNIPROT:P42218; EMBL:X74567; NID:G397404; PIDN:CAA52659.1; PID:G3974
R;Pazzani, C.; Rosenow, C.; Boulnois, G.J.; Bromer, D.; Jann, K.; Roberts, I.S.
J. Bacteriol. 175, 5978-5983, 1993
A;Title: Molecular analysis of region 1 of the Escherichia coli K5 antigen gene cluster:
A;Reference number: A48492; MUID:93388530; PMID:8397187
A;Accession: E48492
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 22-389 <PAZ>
A;Cross-references: GB:X74567
R;Steenbergen, S.M.; Wrona, T.J.; Vimr, E.R.
J. Bacteriol. 174, 1099-1108, 1992
A;Title: Functional analysis of the stalylttransferase complexes in Escherichia coli K1 a
A;Reference number: A42644; MUID:92138601; PMID:1735705
A;Accession: C42644
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 106-125, 'D', 127-244, 'N', 246-297, 'S', 299-300, 'VI', 303-379, 'M', 381-385, 'W', 387
A;Cross-references: GB:M76370; NID:G146947; PIDN:AAA24214.1; PID:G146950
A;Experimental source: K1, strain EV1
A;Note: sequence extracted from NCBI backbone (NCBIN:79370, NCBIP:79381)
C;Genetics:
A;Gene: kpsD
C;Superfamily: kpsD protein

Query Match 79.5%; Score 31; DB 1; Length 389;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSSL 8
| | | | |
Db 127 GVNAYSSL 134

RESULT 8
E81286
Probable polysaccharide modification protein Cj1413c [imported] - Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: E81286
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Kertley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barral
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: E81286
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <PAR>
A;Cross-references: UNIPROT:Q9PNP4; GB:AL139078; GB:AL111168; NID:G6969723; PIDN:CAB7383
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj1413c
C;Superfamily: kpsD protein

Query Match 79.5%; Score 31; DB 2; Length 394;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSSL 8
| | | | |
Db 126 GVNAYSSL 133

RESULT 9

D69750
phosphotransferase system enzyme II homolog ybfs - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69750
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
A.; Brnlich, S.D.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Eron, S.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, K.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A59580; MUID:98044033; PMID:9384377
A;Accession: D69750
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-631 <KUN>
A;Cross-references: UNIPROT:P39816; GB:Z99105; GB:AL009126; NID:G2632457; PIDN:CAB12029
A;Experimental source: strain 168
C;Genetics:
A;Gene: ybfs
C;Superfamily: phosphotransferase system N-acetylglucosamine-specific enzyme II; phosph
nzyme II, factor III homolog

Query Match 79.5%; Score 31; DB 2; Length 631;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSSL 8
| | | | |
Db 172 GINAASSL 179

RESULT 10
S48463
SEC24 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein Yil109c
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48463
R;Bowman, S.; Churcher, C.
Submitted to the EMBL Data Library, September 1994
A;Reference number: S48455
A;Accession: S48463
A;Molecule type: DNA
A;Residues: 1-926 <BOW>
A;Cross-references: UNIPROT:P40482; GB:Z47047; EMBL:Z38125; NID:G603997; PID:G763237; G
C;Genetics:
A;Gene: SGD:SEC24; SEC24; MIPS:YIL109C
A;Cross-references: MIPS:YIL109C; SGD:S0001371
A;Map position: 9L
C;Function:
A;Description: involved in endoplasmic reticulum to Golgi transport; required for vesicl

Query Match 79.5%; Score 31; DB 2; Length 926;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VNAXSSLF 9
| | | | |
Db 787 INATSSLF 794

RESULT 11
A99227

hypothetical protein SSO0775 [imported] - Sulfolobus solfataricus
 C:Species: Sulfolobus solfataricus
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C:Accession: A99227
 R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
 arett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.
 A:Reference number: A99139
 A:Accession: A99227
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-109 <KUR>
 A:Cross-references: UNIPROT:Q9UXG2; GB:AE006641; NID:g13813950; PIDN:AAK41072.1; GSPDB:G
 C:Genetics:
 A:Gene: SSO0775

Query Match 76.9%; Score 30; DB 2; Length 109;
 Best Local Similarity 55.6%; Pred. No. 7.7;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSLF 9
 I:|:|:|:|
 DB 99 GINAVKSIF 107

RESULT 12
 AD0105
 probable sugar-binding protein YPO0856 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AD0105
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 al, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AD0105
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-420 <KUR>
 A:Cross-references: UNIPROT:Q8ZHN4; GB:AL590842; PIDN:CAC89703.1; PID:g15978930; GSPDB:G
 C:Genetics:
 A:Gene: YPO0856
 C:Superfamily: maltose-binding protein

Query Match 76.9%; Score 30; DB 2; Length 420;
 Best Local Similarity 66.7%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSLF 9
 I:|:|:|:|
 DB 248 GLNAIDSLF 256

RESULT 13
 T02404
 Probable beta-glucosidase homolog F411.30 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
 C:Accession: T02404; B84879
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, May 1998
 A:Description: Arabidopsis thaliana chromosome II BAC F411 genomic sequence.
 A:Reference number: Z1467
 A:Accession: T02404
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-560 <RCU>
 A:Cross-references: UNIPROT:O64883; EMBL:AC004521; NID:g3128166; PIDN:AAK16095.1; PID:g3
 A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-766, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: B84879
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-560 <STO>
 A:Cross-references: GB:AE002093; NID:g3128191; PIDN:AAK16095.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g44490; F411.30
 A:Map position: 2
 A:Introns: 3/2; 33/3; 76/3; 102/1; 157/2; 242/3; 281/2; 354/1; 400/1; 438/2
 C:Superfamily: Agrobacterium beta-glucosidase

Query Match 76.9%; Score 30; DB 2; Length 560;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSLF 9
 I:|:|:|:|
 DB 322 GINYISLIF 330

RESULT 14
 T27215
 hypothetical protein Y57G11C.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T27215
 R:McMurray, A.
 submitted to the EMBL Data Library, September 1997
 A:Reference number: Z20330
 A:Accession: T27215
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-633 <WIL>
 A:Cross-references: UNIPROT:O18227; EMBL:Z99281; PIDN:CAB16503.1; GSPDB:GN00022; CESP:Y5
 A:Experimental source: clone Y57G11C
 C:Genetics:
 A:Gene: CESP:Y57G11C.1
 A:Map position: 4
 A:Introns: 70/1; 329/3
 C:Superfamily: multidrug resistance protein; ATP-binding cassette homology

Query Match 76.9%; Score 30; DB 2; Length 633;
 Best Local Similarity 75.0%; Pred. No. 54;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSLF 9
 I:|:|:|:|
 DB 328 INAFSSLF 335

RESULT 15
 S58439
 transcription factor AKR - chicken
 N:Alternate names: avian knotted-related protein; homeotic protein AKR
 C:Species: Gallus gallus (chicken)
 C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
 C:Accession: S58439; S58440
 R:Ryan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; Deeley, R.G.
 submitted to the EMBL Data Library, April 1995
 A:Description: Isolation and characterization of the chicken homeodomain protein AKR.
 A:Reference number: S58439
 A:Accession: S58439
 A:Molecule type: mRNA
 A:Residues: 1-269 <RYA>
 A:Cross-references: UNIPROT:Q90655; EMBL:U25353; NID:g857681; PIDN:AAA83567.1; PID:g8576
 R:Ryan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; Deeley, R.G.
 Nucleic Acids Res. 23, 3252-3259, 1995

A;Title: Isolation and characterization of the chicken homeodomain protein AKR.
A;Reference number: S58440; MUID:95396587; PMID:7667102
A;Accession: S58440
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 35-94 <RYP>
A;Cross-references: EMBL:U25353
C;Function:
A;Description: negative regulator of apovLDLII (major egg yolk apolipoprotein)
A;Note: expressed in liver during early embryogenesis and in non-hepatic adult tissues
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;36-95/Domain: homeobox homology <Hox>

Query Match 74.4%; Score 29; DB 2; Length 269;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GVNAXSSLF 9
| | | | |
Db 222 GANACGLF 230

Search completed: October 26, 2004, 16:06:05
Job time : 10.7353 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:50 ; Search time 40.6324 Seconds
(without alignments)
127.445 Million cell updates/sec

Title: US-10-032-950-1

Perfect score: 39

Sequence: 1 GVNAXSSLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt.02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	92.3	47	2 O33586	O33586 staphylococ
2	36	92.3	47	2 Q7A2N4	Q7A2N4 staphylococ
3	36	92.3	47	2 Q7A417	Q7A417 staphylococ
4	36	92.3	47	2 CAE92745	CAE92745 staphyloc
5	36	92.3	47	2 CAE92748	CAE92748 staphyloc
6	36	92.3	47	2 CAE92751	CAE92751 staphyloc
7	36	92.3	47	2 CAE92754	CAE92754 staphyloc
8	36	92.3	47	2 CAE92757	CAE92757 staphyloc
9	35	89.7	189	2 Q922T9	Q922T9 mus musculus
10	35	89.7	406	1 LMP1_MOUSE	L1438 mus musculus
11	35	89.7	406	1 Q8VH34	Q8VH34 mus musculus
12	35	89.7	407	1 LMP1_RAT	R14562 rattus norv
13	35	89.7	407	2 Q9DCI3	Q9DCI3 mus musculus
14	34	87.2	333	2 Q34933	Q34933 bacillus su
15	32	82.1	46	2 Q9FIU5	Q9FIU5 staphylococ
16	32	82.1	895	2 Q9SC24	Q9SC24 arabidopsis
17	32	82.1	895	2 Q94C93	Q94C93 arabidopsis
18	31	79.5	296	2 Q47402	Q47402 escherichia
19	31	79.5	313	2 Q8RU04	Q8RU04 cryza sativ
20	31	79.5	375	2 Q7VGP8	Q7VGP8 helicobacte
21	31	79.5	389	1 KSS5_ECOLI	P42218 escherichia
22	31	79.5	389	2 Q6KCZ9	Q6KCZ9 escherichia
23	31	79.5	389	2 CAE55819	CAE55819 escherich
24	31	79.5	394	2 Q9PMP4	Q9PMP4 campylobact
25	31	79.5	406	2 Q9X5N8	Q9X5N8 escherichia
26	31	79.5	406	2 Q7W6P9	Q7W6P9 bordetella
27	31	79.5	406	2 Q7WIC9	Q7WIC9 bordetella
28	31	79.5	407	1 LMP1_CRIGR	P49129 cricetus
29	31	79.5	408	2 Q8EV24	Q8EV24 mycoplasma
30	31	79.5	412	2 Q8FDP8	Q8FDP8 escherichia
31	31	79.5	469	2 Q6NBU0	Q6NBU0 rhodopseudo

32	31	79.5	469	2 CAE26182	CAE26182 rhodopseu
33	31	79.5	631	1 YBFS_BACSU	P39816 bacillus su
34	31	79.5	783	2 Q9LAW0	Q9LAW0 mycoplasma
35	31	79.5	891	2 Q75B16	Q75B16 ashbya goss
36	31	79.5	891	2 AAS51681	AAS51681 ashbya go
37	31	79.5	926	1 SC24_YEAST	P40482 saccharomyc
38	30	76.9	109	2 Q8UXG2	Q8UXG2 sulfolobus
39	30	76.9	153	2 Q89EV1	Q89EV1 bradyrhizob
40	30	76.9	255	2 Q78BR1	Q78BR1 carassius a
41	30	76.9	255	2 Q98SE3	Q98SE3 carassius a
42	30	76.9	300	2 Q737N6	Q737N6 bacillus ce
43	30	76.9	300	2 AAS41526	AAS41526 bacillus
44	30	76.9	303	2 Q6HIC7	Q6HIC7 bacillus th
45	30	76.9	318	2 Q728M2	Q728M2 emericella

ALIGNMENTS

RESULT 1

O33586 PRELIMINARY; PRT; 47 AA.
AC O33586;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE AgrD.
GN Name=agrD;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1] _
RP SEQUENCE FROM N.A.
RC STRAIN-SA502A.
RX MEDLINE=97342847; PubMed=9197262;
RA Ji G., Beavis R., Novick R.P.;
RT "Bacterial interference caused by autoinducing peptide variants.";
RL Science 276:2027-2030(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Gt31a-cp5, Gt31b-cp5, Gt36a-cp8, Gt36b-cp8, and Gt111-cp8;
RA Goerke C., Dabach S., Kuemmel M., Wolz C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001782; AAB63265.1; -
DR EMBL; AJ617715; CAE92745.1; -
DR EMBL; AJ617716; CAE92748.1; -
DR EMBL; AJ617717; CAE92751.1; -
DR EMBL; AJ617718; CAE92754.1; -
DR EMBL; AJ617719; CAE92757.1; -
DR PIR; C89995; C89995.
DR InterPro; IPR009229; AgrD.
DR Pfam; PF05931; AgrD; 1.
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 92.3%; Score 36; DB 2; Length 47;

Best Local Similarity 88.9%; Fred. No. 1;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSLF 9

|||||
24 GVNACSSLF 32

RESULT 2

Q7A2N4 PRELIMINARY; PRT; 47 AA.
AC Q7A2N4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AgrD protein.
GN Name=agrD; OrderedLocusNames=SAV2037;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).

RC STRAIN=gt36a-cp8;
 RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
 RT "Evolutionary Models for the Development of the Polymorphic Loci agr
 and cap in Staphylococcus aureus";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ617717; CAB92751.1; -;
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 92.3%; Score 36; DB 2; Length 47;
 Best Local Similarity 88.9%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSSLF 9
 |||||
 Db 24 GVNACSSSLF 32

RESULT 7
 CAE92754 PRELIMINARY; PRT; 47 AA.
 ID CAE92754
 AC CAE92754;
 DT 01-APR-2004 (TrEMBLrel. 27, Created)
 DT 01-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 01-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE AGD protein.
 GN AGD.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=gt36b-cp8;
 RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
 RT "Evolutionary Models for the Development of the Polymorphic Loci agr
 and cap in Staphylococcus aureus";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ617718; CAB92754.1; -;
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 92.3%; Score 36; DB 2; Length 47;
 Best Local Similarity 88.9%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSSLF 9
 |||||
 Db 24 GVNACSSSLF 32

RESULT 8
 CAE92757 PRELIMINARY; PRT; 47 AA.
 ID CAE92757
 AC CAE92757;
 DT 01-APR-2004 (TrEMBLrel. 27, Created)
 DT 01-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 01-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE AGD protein.
 GN AGD.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=gt111-cp8;
 RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
 RT "Evolutionary Models for the Development of the Polymorphic Loci agr
 and cap in Staphylococcus aureus";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ617719; CAB92757.1; -;
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 92.3%; Score 36; DB 2; Length 47;
 Best Local Similarity 88.9%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSSLF 9
 |||||
 Db 24 GVNACSSSLF 32

RESULT 9

Q922T9 PRELIMINARY; PRT; 189 AA.
 ID Q922T9
 AC Q922T9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-YAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Lampi protein (Fragment).
 GN Name=Lampi;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udwin T.B., Toshyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Raebigh M., Madan A., Kettner M., Maman A.C., Rodriguez S., Sanchez A.,
 Whiting M., Young A.C., Shevchenko V., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006785; AAH06785.1; -;
 DR MGD; MGI:96745; Lampi.
 DR GO; GO:0005764; C:lysosome; IDA.
 DR GO; GO:0005771; C:multivesicular body; IDA.
 DR GO; GO:0042383; C:sarcolemma; IDA.
 DR InterPro; IPR002000; Lamp.
 DR Pfam; PF01299; Lamp; 1.
 DR PRINTS; PR00336; LYSASOCTDMP.
 DR PROSITE; PS00310; LAMP_1; 1.
 DR PROSITE; PS00311; LAMP_2; 1.
 FT NON TER 1
 SQ SEQUENCE 189 AA; 20456 MW; 71P16D69BA4066FA CRC64;

Query Match

Best Local Similarity 89.7%; Score 35; DB 2; Length 189;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSSLF 9
 |||||
 Db 63 GVNACSSSLF 71

RESULT 10

01-MAR-2002 (TREMELrel. 20, Last sequence update)
01-MAR-2004 (TREMELrel. 26, Last annotation update)
LAMP-1.
Name=Lamp1;
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RA Ono K., Han J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY069968; AAL58070.1; -;
DR MGI; 96745; Lamp1.
DR GO; GO:0005764; C:lysosome; IDA.
DR GO; GO:0005771; C:multivesicular body; IDA.
DR GO; GO:0042383; C:sarcolemma; IDA.
DR InterPro; IPR002000; Lamp.
DR Pfam; PF01299; Lamp; 1.
DR PRINTS; PR00336; LYSASSOCTDMP.
DR PROSITE; PS00310; LAMP_1; 2.
DR PROSITE; PS00311; LAMP_2; 1.
SQ SEQUENCE 406 AA; 43879 MW; CLEBD373548ADFA85 CRC64;
Query Match 89.7%; Score 35; DB 2; Length 406;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GVNAXSSLF 9
Db 280 GVNAXSSLF 288
RESULT 12
ID LMP1_RAT STANDARD; PRT; 407 AA.
AC P14562; P97620;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (120
kDa lysosomal membrane glycoprotein) (LGP-120) (CD107A).
GN Name=Lamp1; Synonyms=Lamp-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89017240; PubMed=3174652;
RA Howe C.L., Granger B.L., Hull M., Green S.A., Gabel C.A., Helenius A.,
Mellman I.;
RT "Derived protein sequence, oligosaccharides, and membrane insertion of
the 120-kDa lysosomal membrane glycoprotein (lgp120): identification
of a highly conserved family of lysosomal membrane glycoproteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:7577-7581(1988).
RN [2]
RP SEQUENCE OF 22-407 FROM N.A.
RX MEDLINE=89153580; PubMed=2920835;
RA Himeno M., Noguchi Y., Sasaki H., Tanaka Y., Furuno K., Kono A.,
Sakai Y., Kato K.;
RT "Isolation and sequencing of a cDNA clone encoding 107 kDa
stialoglycoprotein in rat liver lysosomal membranes.";
RL FEBS Lett. 244:351-356(1989).
RN [3]
RP SEQUENCE OF 283-357 FROM N.A.
RC STRAIN=Wistar Kyoto; TISSUE=Aortic smooth muscle;
RA Adams L.A., Weirny I., Schwartz S.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Presents carbohydrate ligands to selectins. Also
implicated in tumor cell metastasis.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal. This
protein shuttles between lysosomes, endosomes, and the plasma

membrane.
-!- PTM: O- and N-glycosylated; some of the N-glycans attached to
LAMP-1 are polylactosaminoglycans (By similarity).
-!- SIMILARITY: Belongs to the LAMP family.

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DR EMBL; M34959; AAA41525.1; -;
DR EMBL; X14765; CAA32873.1; -;
DR EMBL; U75406; AAB19108.1; -;
DR PIR; A30200; A30200.
DR RGD; 2989; Lamp1.
DR InterPro; IPR002000; Lamp.
DR Pfam; PF01299; Lamp; 1.
DR PRINTS; PR00336; LYSASSOCTDMP.
DR PROSITE; PS00310; LAMP_1; 2.
DR PROSITE; PS00311; LAMP_2; 1.
KW Glycoprotein; Lysosome; Signal; Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 407
Lysosome-associated membrane glycoprotein
1.
FT DOMAIN 22 371
Lumenal (Potential).
FT TRANSMEM 372 395
Potential.
FT DOMAIN 396 407
Cytoplasmic (Potential).
FT DOMAIN 22 189
First lumenal domain.
FT DOMAIN 190 219
Hinge.
FT DOMAIN 220 371
Second lumenal domain.
FT DISULFID 36 75
By similarity.
FT DISULFID 150 186
By similarity.
FT DISULFID 223 260
By similarity.
FT DISULFID 328 365
By similarity.
FT CARBOHYD 32 32
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 59 59
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 71 71
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 79 79
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 102 102
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 116 116
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 125 125
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 145 145
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 150 150
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 178 178
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 215 215
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 220 220
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 233 233
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 241 241
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 271 271
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 283 283
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 297 297
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 312 312
N-linked (GlcNAc. .) (Potential).
FT CONFLICT 293 294
GV -> EF (in Ref. 3).
FT CONFLICT 329 329
N -> T (in Ref. 3).
FT CONFLICT 356 357
SD -> VT (in Ref. 3).
SQ SEQUENCE 407 AA; 43969 MW; 25947490749A7C98 CRC64;
Query Match 89.7%; Score 35; DB 1; Length 407;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GVNAXSSLF 9
Db 281 GVNAXSSLF 289
RESULT 13
Q9DC13
ID Q9DC13 PRELIMINARY; PRT; 407 AA.
AC Q9DC13;

RT of the *Bacillus subtilis* genome reveal genes for a new two-component RT system, three spore germination proteins, an iron uptake system and a general stress response protein."

RL Gene 194:191-199(1997).
 DR EMBL; Z99108; CAB12580.1; -;
 DR EMBL; D86417; BAA22318.1; -;
 DR PIR; C69812; C69812.
 DR HSSP; P06609; 1L7V.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000522; FecD.
 DR Pfam; PF01032; FecD; 1.
 KW Complete proteome.
 SQ SEQUENCE 333 AA; 35098 MW; 9F4BB91BB0BE6761 CRC64;

Query Match 87.2%; Score 34; DB 2; Length 333;
 Best Local Similarity 77.8%; Pred. No. 25;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSLF 9
 |||||:||||
 Db 99 GVNAGSLF 107

RESULT 15

Q9FIUS PRELIMINARY; PRT; 46 AA.
 AC Q9FIUS;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE AgrD.
 DE Name=agrD;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21137858; PubMed=11240104;
 RA Takeuchi S., Maeda T., Hashimoto N., Imaizumi K., Kaidoh T.,
 RA Hayakawa Y.;
 RT "Variation of the agr locus in Staphylococcus aureus isolates from
 cows with mastitis";
 RL Vet. Microbiol. 79:267-274(2001).
 DR EMBL; AB043554; BAB18547.1; -;
 DR InterPro; IPR009229; AgrD.
 DR Pfam; PF05931; AgrD; 1.
 DR PIR; PF05931; AgrD; 1.
 SQ SEQUENCE 46 AA; 5050 MW; 404714CDC4BFA77E CRC64;

Query Match 82.1%; Score 32; DB 2; Length 46;
 Best Local Similarity 77.8%; Pred. No. 8.7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSLF 9
 |||||:||||
 Db 24 GVNACSLF 32

Search completed: October 26, 2004, 16:04:54
 Job time : 43.6324 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:15 ; Search time 42.75 Seconds
(without alignments)
75.522 Million cell updates/sec

Title: US-10-032-950-2

Perfect score: 39

Sequence: 1 GANAXSSLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04.*

1: Geneseqp1980s.*

2: Geneseqp1980s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	94.9	9	3 AAY67852	Aay67852 S. aureus
2	37	94.9	9	5 AAM50900	Aam50900 AgrD-auto
3	37	94.9	9	5 ABP53541	Abp53541 Cyclic pe
4	34	87.2	9	3 AAY67860	Aay67860 Staphyloc
5	34	87.2	9	3 AAY67859	Aay67859 Staphyloc
6	34	87.2	9	5 ABB07160	Abb07160 Peptide-m
7	34	87.2	9	5 AAM50907	Aam50907 Protected
8	34	87.2	9	5 AAM51004	Aam51004 AgrD2 lac
9	34	87.2	9	5 AAM51003	Aam51003 AgrD2 lin
10	34	87.2	9	5 AAM51002	Aam51002 AgrD2 lin
11	33	84.6	9	3 AAY67851	Aay67851 S. aureus
12	33	84.6	9	3 AAY67861	Aay67861 Staphyloc
13	33	84.6	9	5 ABB07161	Abb07161 Peptide-m
14	33	84.6	9	5 AAM51005	Aam51005 AgrD2 lac
15	33	84.6	9	5 AAM50908	Aam50908 Protected
16	33	84.6	9	5 AAM50899	Aam50899 AgrD-auto
17	33	84.6	9	5 ABP53540	Abp53540 Cyclic pe
18	32	82.1	9	2 AAW38323	Aaw38323 Transcrip
19	32	82.1	9	5 ABB07159	Abb07159 Peptide-m
20	32	82.1	9	5 AAM51001	Aam51001 AgrD2 thi
21	32	82.1	9	6 ABB4631	Abb4631 S. aureus
22	32	82.1	9	7 ADF09190	Adf09190 S. aureus
23	32	82.1	9	8 ADJ36875	Adj36875 Peptide t
24	32	82.1	47	6 ABB4634	Abb4634 S. aureus
25	32	82.1	47	7 ADF09193	Adf09193 S. aureus

ALIGNMENTS

RESULT 1

AAY67852

ID AAY67852 standard; peptide; 9 AA.

XX

AC AAY67852;

XX

DT 25-APR-2000 (first entry)

XX

DE S. aureus peptide #2 used for bacterial interference.

XX

XX Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;

KW virulence factor; treatment.

XX

OS Staphylococcus aureus.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal residue forms bond with C-terminal

FT residue to form a cyclic peptide"

FT Misc-difference 5

FT /label= Unknown

XX

PN WO9867286-A2.

XX

PD 29-DEC-1999.

XX

PF 24-JUN-1999; 99WO-US014562.

XX

PR 24-JUN-1998; 98US-00103438.

XX

PA (UYRQ) UNIV ROCKEFELLER.

PA (UYNY) UNIV NEW YORK STATE.

XX

PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX WPI; 2000-147202/13.

XX

PT New cyclic peptides for treating infections with Staphylococcus aureus.

XX

PS Claim 9; Page 26; 37pp; English.

XX

CC This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes

CC with this response in strains of different groups. The peptides and
 CC composition containing them can be used to treat infections by *S. aureus*
 XX
 SQ Sequence 9 AA;

Query Match 94.9%; Score 37; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GANAXSSLF 9
 Db 1 GANAXSSLF 9

RESULT 2
 AAM50900
 ID AAM50900 standard; peptide; 9 AA.

XX AC AAM50900;

XX DT 08-MAY-2002 (first entry)

XX DE AgrD-autoinducing cyclic peptide, inhibitor of agr response.

XX DE Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;

XX KW antibacterial; infection; therapy; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"

FT FT Misc-difference 5 /note= "any amino acid"

FT FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"

XX USG337385-B1.

XX XX 08-JAN-2002.

XX XX 24-JUN-1999; 99US-00339511.

XX XX 24-JUN-1998; 98US-0090402P.

XX XX (UVRQ) UNIV ROCKEFELLER..

XX XX (UVRQ) UNIV NEW YORK STATE.

XX XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX XX WPI; 2002-170774/22.

XX XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial

XX XX interference and for treating Staphylococcus aureus infection in a

XX XX subject.

XX XX Claim 7; Col 19; 18pp; English.

XX The present sequence is that of a novel synthetic cyclic peptide of the
 XX invention that is capable of inhibiting the agr response of
 XX Staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is
 XX a secreted agr-encoded peptide and where the agr locus controls the
 XX synthesis of virulence factor and other extracellular proteins
 XX responsible for pathogenicity in *S. aureus*. Preferred peptides may have
 XX the sequence NH₂-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z
 XX residue and COOH other than a thioester bond, where X is an amino acid,
 XX an amino acid analogue, a peptidomimetic or non-amide isoster, Z is a
 XX synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The
 XX cyclic bond is especially a lactam or lactone bond. The thiolactone
 XX structure within native AgrD peptides is required for activation of the
 XX agr response. Elimination of the thiol ester component of the cyclic ring
 XX structure can destroy agr response activating activity while preserving
 XX and enhancing inhibitory activity. A claimed method of preparing a cyclic

CC peptide involves: assembling a linear peptide chain on to a solid phase
 CC resin support; deprotecting the resulting protected assembled peptide;
 CC treating the deprotected peptide with neutral buffer for a time
 CC sufficient to form the cyclic peptide and cleave the peptide from the
 CC support; and recovering the cyclic peptide. The peptide is useful for
 CC bacterial interference, especially for the treatment of *S. aureus*
 XX infection
 XX SQ Sequence 9 AA;

Query Match 94.9%; Score 37; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GANAXSSLF 9
 Db 1 GANAXSSLF 9

RESULT 3
 ABP53541
 ID ABP53541 standard; peptide; 9 AA.

XX AC ABP53541;

XX DT 13-DEC-2002 (first entry)

XX DE Cyclic peptide SEQ ID NO:2.

XX KW Cyclic peptide; Staphylococcus aureus; infection; antibacterial;

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 5 /note= "any amino acid"

XX US2002077453-A1.

XX XX 20-JUN-2002.

XX XX 27-DEC-2001; 2001US-00032950.

XX XX 24-JUN-1998; 98US-0090402P.

XX XX 24-JUN-1999; 99US-00339511.

XX XX (MUIR/) MUIR T W.

XX XX (MAYV/) MAYVILLE P.

XX XX (NOVI/) NOVICK R P.

XX XX (BEAV/) BEAVIS R.

XX XX (JIGG/) JI G.

XX XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX XX WPI; 2002-681366/73.

XX XX New cyclic peptides, useful for treating Staphylococcus aureus

XX XX infections.

XX XX Claim 9; Page 10; 18pp; English.

XX ABP53540 to ABP53547 represent cyclic peptides (I) from the present
 XX invention. The present invention also describes a method for treating
 XX Staphylococcus aureus infection comprising the administration of a
 XX composition comprising (I). (I) has antibacterial activity, and can be
 XX used as an agr gene response inhibitor. The peptides are useful for
 XX treating *S. aureus* infections

XX SQ Sequence 9 AA;

Query Match 94.9%; Score 37; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
 DB 1 GANAXSSLF 9

RESULT 4
 AAY67860
 ID AAY67860 standard; peptide; 9 AA.
 XX
 AC AAY67860;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Staphylococcus aureus AgrDII derived peptide sequence.
 XX
 KW Staphylococcus aureus infection; AgrD; agr response; treatment;
 KW virulence factor.
 XX
 OS Staphylococcus aureus.
 XX
 FN WO9967286-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 24-JUN-1999; 99WO-US014562.
 XX
 PR 24-JUN-1998; 98US-00103438.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 PA (UYNV) UNIV NEW YORK STATE.
 XX
 PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;
 XX
 DR WPI; 2000-147202/13.
 XX
 PT New cyclic peptides for treating infections with Staphylococcus aureus.
 XX
 PS Example; Page 22; 37pp; English.
 XX
 CC This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus

Query Match 87.2%; Score 34; DB 3; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
 DB 1 GVNAXSSLF 9

RESULT 5
 AAY67859
 ID AAY67859 standard; peptide; 9 AA.
 XX
 AC AAY67859;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Staphylococcus aureus AgrDII derived peptide sequence.
 XX
 KW Staphylococcus aureus infection; treatment; AgrD; agr response;

Query Match 87.2%; Score 34; DB 3; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
 DB 1 GVNAXSSLF 9

RESULT 6
 ABB07160
 ID ABB07160 standard; peptide; 9 AA.
 XX
 AC ABB07160;
 XX
 DT 13-MAR-2002 (first entry)
 XX
 DE Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
 XX
 KW Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
 KW vulnery; pheromone; agr system; accessory gene regulator; cyclic.
 XX
 OS Synthetic.
 XX
 FN WO200185664-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-US015221.
 XX
 PR 10-MAY-2000; 2000US-0203000P.
 PR 07-DEC-2000; 2000US-0254398P.
 XX
 PA (UYPR-) UNIV PRINCETON.
 PA (QUOR-) CJOOREX PHARM INC.
 PA (UYTE-) UNIV TECHNOLOGIES INT INC.
 XX
 PI Bassler BL, Dammel CS, Schauder S, Shokat K, Stein J, Surette MG;

virulence factor.
 XX
 OS Staphylococcus aureus.
 XX
 FN WO9967286-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 24-JUN-1999; 99WO-US014562.
 XX
 PR 24-JUN-1998; 98US-00103438.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 PA (UYNV) UNIV NEW YORK STATE.
 XX
 PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;
 XX
 DR WPI; 2000-147202/13.
 XX
 PT New cyclic peptides for treating infections with Staphylococcus aureus.
 XX
 PS Example; Page 22; 37pp; English.
 XX
 CC This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus

Query Match 87.2%; Score 34; DB 3; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
 DB 1 GVNAXSSLF 9

RESULT 6
 ABB07160
 ID ABB07160 standard; peptide; 9 AA.
 XX
 AC ABB07160;
 XX
 DT 13-MAR-2002 (first entry)
 XX
 DE Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
 XX
 KW Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
 KW vulnery; pheromone; agr system; accessory gene regulator; cyclic.
 XX
 OS Synthetic.
 XX
 FN WO200185664-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-US015221.
 XX
 PR 10-MAY-2000; 2000US-0203000P.
 PR 07-DEC-2000; 2000US-0254398P.
 XX
 PA (UYPR-) UNIV PRINCETON.
 PA (QUOR-) CJOOREX PHARM INC.
 PA (UYTE-) UNIV TECHNOLOGIES INT INC.
 XX
 PI Bassler BL, Dammel CS, Schauder S, Shokat K, Stein J, Surette MG;

XX (UYRQ) UNIV ROCKEFELLER.
PA (UYNV) UNIV NEW YORK STATE.
XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX WPI; 2002-170774/22.
XX
XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
PT interference and for treating Staphylococcus aureus infection in a
PT subject.
XX
XX Example 1; Col 9; 18pp; English.
XX
XX The present sequence is that of a novel synthetic AgrD2 lactone cyclic
CC peptide in which residue 5 of the peptide is linked to residue 9 via a
CC lactone bond. The peptide is derived from an AgrD2 peptide of
CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
CC where the agr locus controls the synthesis of virulence factor and other
CC extracellular proteins responsible for pathogenicity in S. aureus. The
CC biological activity of the synthetic peptide was assayed using cultured
CC S. aureus strains containing a beta-lactamase reporter gene fused to the
CC agrP3 promoter. This allowed activation or inhibition of the agr response
CC to be monitored spectrophotometrically. The lactone AgrD2 peptide
CC inhibited the agr response of group I S. aureus strains without
CC activating the agr response in group I, II or III strains. The invention
CC provides claimed cyclic peptides (see AAM50899-906 and AAM50999) and
CC methods for preparing them, especially peptides where the cyclic bond is
CC a lactam or lactone bond. The cyclic peptides are useful for bacterial
CC interference, especially for the treatment of S. aureus infection.
XX (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 9 AA;

Query Match 87.2%; Score 34; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GANAXSSLF 9
Db 1 GVNASSSLF 9

RESULT 9
AAM51003
ID AAM51003 standard; peptide; 9 AA.
XX
AC AAM51003;
XX
DT 08-MAY-2002 (first entry)
XX
DE AgrD2 linear free acid peptide.
XX
XX AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
KW therapy.
KW Staphylococcus aureus.
XX Synthetic.
OS
OS Staphylococcus aureus.
XX
XX US6337385-B1.
XX
XX 08-JAN-2002.
XX
XX 24-JUN-1999; 99US-00339511.
XX
XX 24-JUN-1998; 98US-0090402P.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX (UYNV) UNIV NEW YORK STATE.
XX
XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX WPI; 2002-170774/22.
XX

XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
PT interference and for treating Staphylococcus aureus infection in a
PT subject.
XX
XX Example 1; Col 9; 18pp; English.
XX
XX The present sequence is that of a novel synthetic AgrD2 linear free acid
CC peptide. The peptide is derived from the cyclic AgrD2 peptide of
CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
CC where the agr locus controls the synthesis of virulence factor and other
CC extracellular proteins responsible for pathogenicity in S. aureus. The
CC biological activity of the synthetic peptide was assayed using cultured
CC S. aureus strains containing a beta-lactamase reporter gene fused to the
CC agrP3 promoter. This allowed activation or inhibition of the agr response
CC to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone
CC cyclic peptide (see AAM51001), the present peptide was unable to either
CC activate or inhibit the agr response, even when added to cultured cells
CC at 100 concentrations. The invention provides claimed cyclic peptides (see
CC AAM50899-906 and AAM50999) and methods for preparing them. The cyclic
CC peptides are useful for bacterial interference, especially for the
CC treatment of S. aureus infection
XX
SQ Sequence 9 AA;

Query Match 87.2%; Score 34; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GANAXSSLF 9
Db 1 GVNASSSLF 9

RESULT 10
AAM51002
ID AAM51002 standard; peptide; 9 AA.
XX
AC AAM51002;
XX
DT 08-MAY-2002 (first entry)
XX
DE AgrD2 linear thioester peptide.
XX
XX AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
KW therapy.
KW Staphylococcus aureus.
XX Synthetic.
OS
OS Key Location/Qualifiers
FH Modified-site 9 /note= "C-terminal thioester"
FT
XX US6337385-B1.
XX
XX 08-JAN-2002.
XX
XX 24-JUN-1999; 99US-00339511.
XX
XX 24-JUN-1998; 98US-0090402P.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX (UYNV) UNIV NEW YORK STATE.
XX
XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX WPI; 2002-170774/22.
XX
XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
PT interference and for treating Staphylococcus aureus infection in a
PT subject.
XX

PS Example 1, Col 9; 18pp; English.

XX The present sequence is that of a novel synthetic AgrD2 linear thioester

CC peptide. The peptide is derived from the cyclic AgrD2 peptide of

CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,

CC where the agr locus controls the synthesis of virulence factor and other

CC extracellular proteins responsible for pathogenicity in *S. aureus*. The

CC biological activity of the synthetic peptide was assayed using cultured

CC *S. aureus* strains containing a beta-lactamase reporter gene fused to the

CC agrP3 promoter. This allowed activation or inhibition of the agr response

CC to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone

CC cyclic peptide (see AAM51001), the present peptide was unable to either

CC activate or inhibit the agr response, even when added to cultured cells

CC at μ M concentrations. The invention provides claimed cyclic peptides (see

CC AAM50899-906 and AAM50999) and methods for preparing them. The cyclic

CC peptides are useful for bacterial interference, especially for the

CC treatment of *S. aureus* infection

XX

SQ Sequence 9 AA;

Query Match 87.2%; Score 34; DB 5; Length 9;

Best Local Similarity 77.8%; Pred. No. 1.7e+06;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GANAXSSSLF 9

Db 1 GVNAAASSLF 9

RESULT 11

AAy67851

ID AAY67851 standard; peptide; 9 AA.

XX

AC AAY67851;

XX

DT 25-APR-2000 (first entry)

XX

DE *S. aureus* peptide #1 used for bacterial interference.

XX

KW Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;

KW virulence factor; treatment.

XX

OS Staphylococcus aureus.

XX

PH Key Location/Qualifiers

FT Misc-difference 5 /label= Unknown

XX

PN WO9967286-A2.

XX

PD 29-DEC-1999.

XX

PF 24-JUN-1999; 99WO-US014562.

XX

PR 24-JUN-1998; 98US-00103438.

XX

PA (UYRQ) UNIV ROCKEFELLER.

PA (UYNY) UNIV NEW YORK STATE.

XX

PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX

DR WPI; 2000-147202/13.

XX

PT New cyclic peptides for treating infections with Staphylococcus aureus.

XX

PS Claim 9; Page 26; 37pp; English.

XX

CC This sequence represents a cyclic peptide derived from the Staphylococcus

CC aureus AgrD peptide. The invention relates to AgrD derived peptides, a

CC composition containing a peptide and a carrier, and a method for the

CC production of the cyclic peptides. The peptide inhibits the agr response,

CC which is normally associated with the release of virulence factors of

CC Staphylococcus aureus. An AgrD peptide is produced by *S. aureus* that

CC activates the agr response in strains of a single group, but interferes

CC with this response in strains of different groups. The peptides and

CC composition containing them can be used to treat infections by *S. aureus*

XX

CC activates the agr response in strains of a single group, but interferes

CC with this response in strains of different groups. The peptides and

CC composition containing them can be used to treat infections by *S. aureus*

XX

SQ Sequence 9 AA;

Query Match 84.6%; Score 33; DB 3; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.7e+06;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GANAXSSSLF 9

Db 1 GVNAXSSSLF 9

RESULT 12

AAy67861

ID AAY67861 standard; peptide; 9 AA.

XX

AC AAY67861;

XX

DT 25-APR-2000 (first entry)

XX

DE Staphylococcus aureus AgrDII derived peptide sequence.

XX

KW Staphylococcus aureus infection; AgrD; agr response; treatment;

KW virulence factor.

XX

OS Staphylococcus aureus.

XX

PH Key Location/Qualifiers

FT Misc-difference 5 /label= Unknown

XX

PN WO9967286-A2.

XX

PD 29-DEC-1999.

XX

PF 24-JUN-1999; 99WO-US014562.

XX

PR 24-JUN-1998; 98US-00103438.

XX

PA (UYRQ) UNIV ROCKEFELLER.

PA (UYNY) UNIV NEW YORK STATE.

XX

PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX

DR WPI; 2000-147202/13.

XX

PT New cyclic peptides for treating infections with Staphylococcus aureus.

XX

PS Example; Page 22; 37pp; English.

XX

CC This sequence represents the Staphylococcus aureus AgrDII derived

CC peptide. The invention relates to AgrD derived cyclic peptides, a

CC composition containing a peptide and a carrier, and a method for the

CC production of the cyclic peptides. The peptide inhibits the agr response,

CC which is normally associated with the release of virulence factors of

CC Staphylococcus aureus. An AgrD peptide is produced by *S. aureus* that

CC activates the agr response in strains of a single group, but interferes

CC with this response in strains of different groups. The peptides and

CC composition containing them can be used to treat infections by *S. aureus*

XX

SQ Sequence 9 AA;

Query Match 84.6%; Score 33; DB 3; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.7e+06;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GANAXSSSLF 9

Db 1 GVNAXSSSLF 9

RESULT 13

ABB07161
ID ABB07161 standard; peptide; 9 AA.

AC ABB07161;
XX

DT 13-MAR-2002 (first entry)
XX

DE Peptide-mediated quorum sensing inhibitor peptide cyclo-XIII.
XX

XX Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
KW vulnary; pheromone; agr system; accessory gene regulator; cyclic.
XX Synthetic.
XX

FH Key Location/Qualifiers
FT Modified-site 5 /note= "diaminoprionic acid residue"

FT
XX WO200185664-A2.
XX

XX 15-NOV-2001.
XX

XX 10-MAY-2001; 2001WO-US015221.
XX

XX 10-MAY-2000; 2000US-0203000P.
PR 07-DEC-2000; 2000US-0254398P.

XX (UYPR-) UNIV PRINCETON.
PA (QUOR-) QUOREX PHARM INC.

XX (UYTE-) UNIV TECHNOLOGIES INT INC.
XX

XX Bassler BL, Dammel CS, Schauder S, Shokat K, Stein J, Surette MG;
PI WPI; 2002-075235/10.
XX

XX Use of autoinducer-2 agonists or antagonists for regulating activity of
PT autoinducer-2 receptor; regulating bacterial growth and pathogenesis,
FT also antibiotic compositions.
XX

XX Disclosure; Page 33; 134pp; English.
XX

XX The invention relates to the use of autoinducer-2 (AI-2) agonists or
CC antagonists for regulating activity of autoinducer-2 receptor, regulating
CC bacterial growth and pathogenesis. Synergistic antibiotic compositions
CC comprising inhibitors of the quorum-sensing pathway of a microorganism
CC are also provided. Methods using such AI-2 analogues are useful for
CC treating pathogen-associated disease states. The compounds and antibiotic
CC compositions can be used to inhibit bacterial cell growth and/or biofilm
CC formation on a medical device, particularly for promoting growth of skin
CC graft replacements used in the treatment of burns and ulcers. They may
CC also be used to aid wound repair, and to inhibit bacterial cell growth
CC and biofilm formation in or on products or devices used for personal
CC hygiene. The present sequence represents an inhibitor of peptide-mediated
CC quorum sensing
XX

SQ Sequence 9 AA;

Query Match 84.6%; Score 33; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9
DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9
DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9
DB 1 GVNAXSSLF 9

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DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9
DB 1 GVNAXSSLF 9

XX

DT 07-AUG-2003 (revised)

DT 08-MAY-2002 (first entry)

XX AgrD2 lactam cyclic peptide.

XX AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;

KW therapy; cyclic.

XX Staphylococcus aureus.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 5

FT /note= "note linked to residue 9 to form cyclic peptide"

FT Misc-difference 5

FT /note= "any amino acid"

FT Misc-difference 9

FT /note= "note linked to residue 5 to form cyclic peptide"

XX US6337385-B1.

XX 08-JAN-2002.

XX 24-JUN-1999; 99US-00339511.

XX 24-JUN-1998; 98US-0090402P.

XX (UYRQ) UNIV ROCKEFELLER.

XX (UYNY) UNIV NEW YORK STATE.

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX WPI; 2002-170774/22.

XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial

PT interference and for treating Staphylococcus aureus infection in a

PT subject.

XX Example 1; Col 11; 18pp; English.

XX The present sequence is that of a novel synthetic AgrD2 lactam cyclic

CC peptide in which residue 5 of the peptide is linked to residue 9 via a

CC lactam bond. The peptide is derived from an AgrD2 peptide of

CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,

CC where the agr locus controls the synthesis of virulence factor and other

CC extracellular proteins responsible for pathogenicity in S. aureus. The

CC biological activity of the synthetic peptide was assayed using cultured

CC S. aureus strains containing a beta-lactamase reporter gene fused to the

CC agrP3 promoter. This allowed activation or inhibition of the agr response

CC to be monitored spectrophotometrically. The AgrD3 lactam peptide

CC inhibited the agr response in group I S. aureus strains and did not

CC activate the agr response in group II or III strains. The invention

CC provides claimed cyclic peptides (see AAM50899-906 and AAM50999) and

CC methods for preparing them, especially where the cyclic bond is a lactam

CC or lactone bond. The cyclic peptides are useful for bacterial

CC interference, especially for the treatment of S. aureus infection.

CC (Updated on 07-AUG-2003 to correct OS field.)

XX Sequence 9 AA;

Query Match 84.6%; Score 33; DB 5; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.7e+06;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9

DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9

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DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9

DB 1 GVNAXSSLF 9

RESULT 15

AAM50908

ID AAM50908 standard; peptide; 9 AA.

XX AAM50908;
XX 08-MAY-2002 (first entry)
XX Protected peptide used in cyclic peptide production.
XX Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
KW antibacterial; infection; therapy; cyclic.
XX Synthetic.
XX OS
XX Key Location/Qualifiers
FH Modified-site 1 /note= "Z-Gly"
FT
FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"
FT Modified-site 5 /label= Dpr(Boc)
FT Modified-site 6 /note= "Ser(Bzl)"
FT Modified-site 7 /note= "Ser(Bzl)"
FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"
XX US6337385-B1.
XX
XX PD 08-JAN-2002.
XX PF 24-JUN-1999; 99US-00339511.
XX PR 24-JUN-1998; 98US-0090402P.
XX PA (UYRQ) UNIV ROCKEFELLER.
XX PA (UYN) UNIV NEW YORK STATE.
XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX WPI; 2002-170774/22.
XX
XX PT Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
FT interference and for treating Staphylococcus aureus infection in a
PT subject.
XX
XX PS Disclosure; Col 14; 18pp; English.
XX
XX The present sequence is that of a protected peptide used in an example of
CC the preparation of novel synthetic cyclic peptides of the invention (see
CC AAM50899-906). The peptide corresponds to the Staphylococcus aureus
CC AgrDII sequence with a Cys to diaminopropionic acid (Dpr) mutation
CC (lactam). It was synthesised on a Wang-resin using an Fmoc N-alpha
CC protection strategy. Following chain assembly, the peptide was cleaved
CC from the support and the Dpr-5 residue deprotected by treatment with a
CC trifluoroacetic acid:anisole:water mixture (90:5:5) for 4 hr. The
CC partially protected peptide-alpha carboxylates were then dissolved in DMF
CC and treated with PyBOP. Cyclization was complete after 2 hr. The
CC remaining protecting groups were removed by treatment with HF and the
CC peptide purified by HPLC. The cyclic peptide is capable of inhibiting the
CC agr response of Staphylococcus aureus. The thiolactone structure within
CC native AgrD peptides is required for activation of this response.
CC Replacement of the thiol ester component of the cyclic ring structure
CC with a lactam (as in the present case) or a lactone can destroy agr
CC response activating activity while preserving and enhancing inhibitory
CC activity. The cyclic peptides are useful for bacterial interference,
CC especially for the treatment of S. aureus infection
XX
XX SQ Sequence 9 AA;

Query Match 84.6%; Score 33; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. NC. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GANAXSSLF 9
Db 1 GVNAXSSLF 9

Search completed: October 26, 2004, 15:59:40
Job time : 44.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:54:00 ; Search time 31.5 Seconds
(without alignments)
92.502 Million cell updates/sec

Title: US-10-032-950-2

Perfect score: 39

Sequence: 1 GANXSSLP 9

Scoring table: BLOSUN62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	37	94.9	9	13	US-10-032-950-2
2	33	84.6	9	13	US-10-032-950-1
3	32	82.1	9	14	US-10-201-444-3
4	32	82.1	47	14	US-10-201-444-6
5	31	79.5	340	15	US-10-425-114-72514
6	31	79.5	498	15	US-10-282-122A-48898
7	31	79.5	1203	16	US-10-437-963-120758
8	31	79.5	1804	16	US-10-437-963-11282
9	30	76.9	9	13	US-10-032-950-5
10	30	76.9	9	13	US-10-032-950-6
11	30	76.9	121	15	US-10-425-114-47226
12	30	76.9	205	15	US-10-424-599-161196
13	30	76.9	247	15	US-10-424-599-161195

14	30	76.9	258	14	US-10-368-687-30	Sequence 30, Appl
15	30	76.9	258	14	US-10-368-687-32	Sequence 32, Appl
16	401	76.9	401	16	US-10-437-963-190543	Sequence 190543,
17	30	76.9	672	14	US-10-368-687-26	Sequence 26, Appl
18	30	76.9	672	14	US-10-368-687-28	Sequence 28, Appl
19	30	76.9	771	16	US-10-487-685-11	Sequence 11, Appl
20	30	76.9	1569	13	US-10-108-805-303	Sequence 303, App
21	29	74.4	60	15	US-10-424-599-190059	Sequence 190059,
22	29	74.4	70	16	US-10-437-963-151008	Sequence 151008,
23	29	74.4	71	16	US-10-767-701-59048	Sequence 59048, A
24	29	74.4	81	14	US-10-016-349A-153	Sequence 153, App
25	29	74.4	109	16	US-10-767-701-38573	Sequence 38573, A
26	29	74.4	122	11	US-09-864-408A-7538	Sequence 7538, Ap
27	29	74.4	129	15	US-10-424-599-269854	Sequence 269854,
28	29	74.4	135	15	US-10-425-114-45245	Sequence 45245, A
29	29	74.4	195	16	US-10-767-701-54464	Sequence 54464, A
30	29	74.4	255	14	US-10-083-357-1280	Sequence 1280, Ap
31	29	74.4	273	15	US-10-425-114-64933	Sequence 64933, A
32	29	74.4	322	15	US-10-425-114-47019	Sequence 47019, A
33	29	74.4	419	15	US-10-425-114-65481	Sequence 65481, A
34	29	74.4	419	15	US-10-425-114-68077	Sequence 68077, A
35	29	74.4	425	15	US-10-425-114-63576	Sequence 63576, A
36	29	74.4	491	14	US-10-094-749-2461	Sequence 2461, Ap
37	29	74.4	550	14	US-10-156-761-11286	Sequence 11286, A
38	29	74.4	971	16	US-10-437-963-168200	Sequence 168200,
39	29	74.4	1066	16	US-10-437-963-164712	Sequence 164712,
40	29	74.4	1218	14	US-10-158-428-2	Sequence 2, Appli
41	29	74.4	1218	15	US-10-432-613-3	Sequence 3, Appli
42	29	74.4	2124	15	US-10-389-647-497	Sequence 497, App
43	28	71.8	9	13	US-10-032-950-7	Sequence 7, Appli
44	28	71.8	25	16	US-10-416-249-492	Sequence 492, App
45	28	71.8	54	15	US-10-424-599-174213	Sequence 174213,

ALIGNMENTS

RESULT 1
US-10-032-950-2
; Sequence 2, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-2

Query Match 94.9%; Score 37; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GANXSSLP 9

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Db      1  GANAXSSLF 9
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US-10-032-950-1
; Sequence 1, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; FILE REFERENCE: 600-1-231N
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: US/10/032,950
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: xaa represents any amino acid at this position.
US-10-032-950-1
Query Match      84.6%; Score 33; DB 13; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1  GANAXSSLF 9
|||||
Db      1  GVNAXSSLF 9
|||||
RESULT 3
US-10-201-444-3
; Sequence 3, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/10/201,444
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-3
Query Match      82.1%; Score 32; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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|||||
Db      1  GVNAXSSLF 9
|||||
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; Sequence 6, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-6
Query Match      82.1%; Score 32; DB 14; Length 47;
Best Local Similarity 77.8%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1  GANAXSSLF 9
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RESULT 5
US-10-425-114-72514
; Sequence 72514, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72514
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-2MFLMO17229E06_FLI.pep
US-10-425-114-72514
Query Match      79.5%; Score 31; DB 15; Length 340;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1  GANAXSSL 8
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Db      66 GANALSSL 73
|||||
RESULT 6
US-10-282-122A-48898
; Sequence 48898, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
```

APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48898
LENGTH: 498
TYPE: PRT
ORGANISM: Bacteroides fragilis
US-10-282-122A-48898

Query Match 79.5%; Score 31; DB 15; Length 498;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
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Db 419 GANAATKLF 427

RESULT 7
US-10-437-963-120758
; Sequence 120758, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 120758
LENGTH: 1203
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Clone ID: PAT_MRT4530_2384C.1.pep
US-10-437-963-120758

Query Match 79.5%; Score 31; DB 16; Length 1203;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
||||:|
Db 929 GANAVASVF 937

RESULT 8
US-10-437-963-111282
; Sequence 111282, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 111282
LENGTH: 1804
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_15275C.1.pep
US-10-437-963-111282

Query Match 79.5%; Score 31; DB 16; Length 1804;
Best Local Similarity 66.7%; Pred. No. 7.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
||||:|
Db 712 GANALATLF 720

RESULT 9
US-10-032-950-5
; Sequence 5, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-5

Query Match 76.9%; Score 30; DB 13; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
| | | | |
DB 1 GVNAXASLF 9

RESULT 10

US-10-032-950-6

; Sequence 6, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 607090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-6

Query Match 76.9%; Score 30; DB 13; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
| | | | |
DB 1 GVNAXASLF 9

RESULT 11

US-10-425-114-47226

; Sequence 47226, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47226

; LENGTH: 121
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3115-032-H10_FLI.pep
US-10-425-114-47226

Query Match 76.9%; Score 30; DB 15; Length 121;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
| | | | |
DB 28 GASAFSSMF 36

RESULT 12

US-10-424-599-161196
; Sequence 161196, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 161196
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_116578C.1.pep
US-10-424-599-161196

Query Match 76.9%; Score 30; DB 15; Length 205;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSL 8
| | | | |
DB 50 GANATSSI 57

RESULT 13

US-10-424-599-161195
; Sequence 161195, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 161195
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_116577C.1.pep
US-10-424-599-161195

Query Match 76.9%; Score 30; DB 15; Length 247;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;

Search completed: October 26, 2004, 16:10:10
Job time : 32.5 secs

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSL 8
Db 55 GANATSSI 62

RESULT 14

US-10-368-687-30
; Sequence 30, Application US/10368687
; Publication No. US20030162713A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alex
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20030162713A1el Human Transporter Proteins
; FILE REFERENCE: 8535-041-999
; CURRENT APPLICATION NUMBER: US/10/368,687
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US/09/556,916
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-368-687-30

Query Match 76.9%; Score 30; DB 14; Length 258;

Best Local Similarity 66.7%; Pred.No. 1.5e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
Db 150 GASALSSMF 158

RESULT 15

US-10-368-687-32
; Sequence 32, Application US/10368687
; Publication No. US20030162713A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alex
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20030162713A1el Human Transporter Proteins
; FILE REFERENCE: 8535-041-999
; CURRENT APPLICATION NUMBER: US/10/368,687
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US/09/556,916
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-368-687-32

Query Match 76.9%; Score 30; DB 14; Length 258;

Best Local Similarity 66.7%; Pred.No. 1.5e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
Db 150 GASALSSMF 158

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:46:55 ; Search time 8.73529 Seconds
(without alignments)
99.132 Million cell updates/sec

Title: US-10-032-950-2

Perfect score: 39

Sequence: 1 GANAXSSLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

FIR 79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	84.6	269	2 S58439	transcription fact
2	33	84.6	382	2 A28067	lysosomal membrane
3	33	84.6	405	2 A60534	P2B/LAMP-1 precurs
4	33	84.6	407	2 A30200	120K lysosomal mem
5	32	82.1	47	2 C89935	AgrD protein [impo
6	32	82.1	453	1 ZBPOC2	ubiquinol-cytochro
7	32	82.1	573	2 F81313	peptidase (M3 fami
8	31	79.5	340	2 S76294	hypothetical prote
9	31	79.5	536	2 T04998	hypothetical prote
10	31	79.5	1232	2 T06165	multidrug resistan
11	30	76.9	213	2 F83144	conserved hypothet
12	30	76.9	250	2 H84428	probable membrane
13	30	76.9	291	2 C89103	protein C18B10.10
14	30	76.9	333	1 C69812	ferrichrome ABC tr
15	30	76.9	895	2 T45786	receptor-protein k
16	29	74.4	313	2 B4725	electron transfer
17	29	74.4	313	2 B85485	probable flavoprot
18	29	74.4	313	2 E30634	probable flavoprot
19	29	74.4	342	2 B85757	partial probable o
20	29	74.4	457	2 A99862	probable outer mem
21	29	74.4	476	2 D86306	Similar to Cytochr
22	29	74.4	551	2 C84549	probable ubiquitin
23	29	74.4	870	2 S74291	hypothetical prote
24	29	74.4	1435	2 T32930	hypothetical prote
25	29	74.4	2124	2 H83357	probable non-ribos
26	28	71.8	171	2 T16158	hypothetical prote
27	28	71.8	186	2 B87290	hypothetical prote
28	28	71.8	211	2 A80899	conserved hypothet
29	28	71.8	226	2 D65105	hypothetical 24.8

30	28	71.8	226	2 D85978	hypothetical prote
31	28	71.8	226	2 A98133	hypothetical prote
32	28	71.8	344	2 S64931	hypothetical prote
33	28	71.8	362	2 A84187	hypothetical prote
34	28	71.8	420	2 AD0105	probable sugar-bin
35	28	71.8	429	2 B71307	conserved hypothet
36	28	71.8	453	2 S57097	indoleamine-pyrrol
37	28	71.8	453	2 T24127	probable chitinase
38	28	71.8	486	2 G96713	probable DNA-bind
39	28	71.8	513	2 T05210	hypothetical prote
40	28	71.8	546	2 B85398	hypothetical prote
41	28	71.8	715	2 T41402	hypothetical prote
42	28	71.8	926	2 S48463	SEC24 protein - ye
43	28	71.8	1200	2 A81343	DNA-directed DNA p
44	28	71.8	1216	2 T02146	costomer complex a
45	28	71.8	1938	2 A37361	probable integral

ALIGNMENTS

RESULT 1

S58439

transcription factor AKR - chicken

N;Alternate names: avian knotted-related protein; homeotic protein AKR

C;Species: Gallus gallus (chicken)

C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004

C;Accession: S58439; S58440

R;Ryan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; Deeley, R.G.

submitted to the EMBL Data Library, April 1995

A;Description: Isolation and characterization of the chicken homeodomain protein AKR.

A;Reference number: S58439

A;Accession: S58439

A;Molecule type: mRNA

A;Residues: 1-269 <RYA>

A;Cross-references: UNIPROT:Q90655; EMBL:U25353; NID:G857681; PIDN:AAA83567.1; PID:G857

R;Ryan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; Deeley, R.G.

Nucleic Acids Res. 23, 3252-3259, 1995

A;Title: Isolation and characterization of the chicken homeodomain protein AKR.

A;Reference number: S58440; MUID:95396587; PMID:7667102

A;Accession: S58440

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 35-94 <RYF>

A;Cross-references: EMBL:U25353

C;Function:

A;Description: negative regulator of apolipoprotein (major egg yolk apolipoprotein)

A;Note: expressed in liver during early embryogenesis and in non-hepatic adult tissues

C;Superfamily: homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;36-95/Domain: homeobox homology <HOX>

Query Match 84.6%; Score 33; DB 2; Length 269;

Best Local Similarity 77.8%; Pred. No. 3.9;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9

Db 222 GANAQSLF 230

RESULT 2

A28067

lysosomal membrane glycoprotein LAMP-1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C;Accession: A28067

R;Chen, J.W.; Cha, Y.; Yuskel, K.U.; Gracy, R.W.; August, J.T.

J. Biol. Chem. 263, 8754-8758, 1988

A;Title: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprot

A;Reference number: A28067; MUID:88243732; PMID:3379044

A;Accession: A28067

A;Molecule type: mRNA

A;Residues: 1-382 <CHE>
A;Cross-references: UNIPROT:P11438; GB:J03881; NID:G198706; PIDN:AAA39411.1; PID:G293692
A;Note: the authors translated the codon ATT for residue 1 as Leu and CCG for residue 2
C;Superfamily: lysosome-associated membrane protein
C;Keywords: glycoprotein; membrane protein

Query Match 84.6%; Score 33; DB 2; Length 382;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSSLF 9
DB 256 GGNASSSLF 264

RESULT 3
A60534
P2B/LAMP-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A60534
R;Heffernan, M.; Yousefi, S.; Dennis, J.W. -
Cancer Res. 49, 6077-6084, 1989
A;Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastasizing cell line
A;Reference number: A60534; MUID:90002989; PMID:2676155
A;Accession: A60534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-405 <HEF>
A;Cross-references: UNIPROT:P11438
C;Superfamily: lysosome-associated membrane protein

Query Match 84.6%; Score 33; DB 2; Length 405;
Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSSLF 9
DB 279 GGNASSSLF 287

RESULT 4
A30200
120K lysosomal membrane glycoprotein precursor - rat
N;Alternate names: sialoglycoprotein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: A30200; S03331
R;Howe, C.L.; Granger, B.L.; Hull, M.; Green, S.A.; Helenius, A.; Mellman, M.; Proc. Natl. Acad. Sci. U.S.A. 85, 7577-7581, 1988
A;Title: Derived protein sequence, oligosaccharides, and membrane insertion of the 120-K glycoproteins.
A;Reference number: A30200; MUID:89017240; PMID:3174552
A;Accession: A30200
A;Molecule type: mRNA
A;Residues: 1-407 <HOW>
A;Cross-references: UNIPROT:P14562; EMBL:J03672
A;Note: the authors translated the codon GGG for residue 15 as Val
R;Himeno, M.; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, K.; Kono, A.; Sakaki, Y.; Kat
FEBS Lett. 244, 351-356, 1989
A;Title: Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in
A;Reference number: S03331; MUID:89153580; PMID:2920835
A;Accession: S03331
A;Molecule type: mRNA
A;Residues: 22-407 <HIM>
A;Cross-references: EMBL:X14765; NID:G56577; PIDN:CAA32873.1; PID:G56578
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Superfamily: lysosome-associated membrane protein
C;Keywords: glycoprotein; membrane protein
F:22-407/Product: lysosomal membrane glycoprotein, 107K #status experimental <MAT>

Query Match 84.6%; Score 33; DB 2; Length 407;
Best Local Similarity 77.8%; Pred. No. 6;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSSLF 9
DB 281 GGNATSSSLF 289

RESULT 5
C89995
AgrD protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89995
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89995
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-47 <KUR>
A;Cross-references: UNIPROT:O33586; GB:BA000018; PID:GL3701831; PIDN:BA843124.1; GSPDB:C
A;Experimental source: strain N315
C;Genetics:
A;Gene: agrD

Query Match 82.1%; Score 32; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSSLF 9
DB 24 GYNACSSSLF 32

RESULT 6
ZPEOC2
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: S16221; S14093
R;Gencic, S.; Schaeffer, H.; von Jagow, G.
Eur. J. Biochem. 199, 123-131, 1991
A;Title: Core I protein of bovine ubiquinol-cytochrome-c reductase; an additional member
re of the proteins.
A;Reference number: S16220; MUID:91293112; PMID:1712295
A;Accession: S16221
A;Molecule type: mRNA
A;Residues: 1-453 <GEN>
A;Cross-references: UNIPROT:P23004; GB:X59693; NID:G299; PIDN:CAA42214.1; PID:G300
A;Note: part of this sequence, including the amino end of the mature protein, was confir
R;Cocco, I.; Lorusso, M.; Sardanelli, A.M.; Minuto, M.; Ronchi, S.; Tedeschi, G.; Papa,
Eur. J. Biochem. 195, 731-734, 1991
A;Title: Structural and functional characteristics of polypeptide subunits of the bovine
A;Reference number: S14093; MUID:91153313; PMID:1847870
A;Accession: S14093
A;Molecule type: protein
A;Residues: 17, 16-40, 'R', 42-46 <COC>
C;Superfamily: mitochondrial processing peptidase alpha chain
C;Keywords: hydrolase; mitochondrial matrix; mitochondrion; oxidative phosphorylation; c
F:1-14/Domain: transit peptide (mitochondrion) #status predicted <TMP>
F:15-453/Product: ubiquinol-cytochrome-c reductase core protein II #status experimental

Query Match 82.1%; Score 32; DB 1; Length 453;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSSLF 9
DB 302 GSNATSSSLY 310

[illegible]

Db 116 GADAKSSIF 124

RESULT 12

H84428

probable membrane protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: H84428

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.; euss, D.; Nietman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84428

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-250 <STO>

A:Cross-references: UNIPROT:Q9ZUA5; GB:AR002093; NID:G4220472; PIDN:AAD12695.1; GSPDB:GN

C:Genetics:

A:Gene: At2g01770

A:Map position: 2

Query Match 76.9%; Score 30; DB 2; Length 250;

Best Local Similarity 75.0%; Pred. No. 19;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSL 8

Db 58 GANASSSI 65

RESULT 13

C89103

protein C18p10.10 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: C89103

R:Anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological

A:Reference number: A75000; MUID:99069613; PMID:9851916

A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele

A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: C89103

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-291 <STO>

A:Cross-references: GB:chr_V; PIDN:AA25811.1; PID:gl699099; GSPDB:GN00023; CESP:C8B10.

C:Genetics:

A:Gene: C18p10.10

A:Map position: 5

Query Match 76.9%; Score 30; DB 2; Length 291;

Best Local Similarity 66.7%; Pred. No. 22;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9

Db 104 GANSESLF 112

RESULT 14

C69812

ferrichrome ABC transporter (permease) homolog yfmd - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: C69812

R:Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C:Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emerson, P.T.; Encian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallex
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: C69812

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-333 <KUN>

A:Cross-references: UNIPROT:Q34933; GB:Z99108; GB:AL009126; NID:G2633055; PIDN:CAB12580.

A:Experimental source: strain 168

C:Genetics:

A:Gene: yfmd

C:Superfamily: ferrichrome ABC transporter

Query Match 76.9%; Score 30; DB 1; Length 333;

Best Local Similarity 66.7%; Pred. No. 25;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9

Db 99 GVNAGASLF 107

RESULT 15

T45786

receptor-protein kinase-like protein - Arabidopsis thaliana

N:Alternate names: protein F26013.190

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 16-Aug-2004

C:Accession: T45786

R:Deleeny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, December 1999

A:Reference number: Z23013

A:Accession: T45786

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-895

A:Cross-references: UNIPROT:Q9SCZ4; EMBL:AL133452

A:Experimental source: cultivar Columbia; BAC clone F26013

C:Genetics:

A:Map position: 3

A>Note: F26013.190

C:Superfamily: protein kinase homology

Query Match 76.9%; Score 30; DB 2; Length 895;

Best Local Similarity 66.7%; Pred. No. 72;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9

Db 122 GLNATNSLF 130

Search completed: October 26, 2004, 16:06:06

Job time : 9.73529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:50 ; Search time 40.6324 Seconds
(without alignments)
127.445 Million cell updates/sec

Title: US-10-032-950-2
Perfect score: 39
Sequence: 1 GANAXSSLF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	87.2	153	2 Q89EV1	Q89ev1 bradyrhizob
2	33	84.6	130	2 Q6CIU3	Q6ciu3 kluyveromyc
3	33	84.6	189	2 Q92279	Q922t9 mus musculus
4	33	84.6	269	1 AKR_CHICK	Q90655 gallus gall
5	33	84.6	406	1 LMP1_MOUSE	P11438 mus musculus
6	33	84.6	406	2 Q8VH34	Q8vh34 mus musculus
7	33	84.6	407	1 LMP1_RAT	P14562 rattus norv
8	33	84.6	407	2 Q9DC13	Q9dc13 mus musculus
9	33	84.6	410	2 Q6DC11	Q6dc11 erwinia car
10	32	82.1	47	2 Q33866	C33866 staphylococ
11	32	82.1	47	2 Q7A2N4	Q7a2n4 staphylococ
12	32	82.1	47	2 Q7A417	Q7a417 staphylococ
13	32	82.1	47	2 CAE92745	Ca92745 staphyloc
14	32	82.1	47	2 CAE92748	Ca92748 staphyloc
15	32	82.1	47	2 CAE92751	Ca92751 staphyloc
16	32	82.1	47	2 CAE92754	Ca92754 staphyloc
17	32	82.1	47	2 CAE92757	Ca92757 staphyloc
18	32	82.1	91	2 Q8W459	Q8w459 arabidopsis
19	32	82.1	453	1 UCR2_BOVIN	P23004 bos taurus
20	32	82.1	573	2 Q9PNJ5	Q9pnj5 campylobact
21	31	79.5	340	2 Q55632	Q55632 synschoyest
22	31	79.5	415	2 Q81552	Q81552 hepatitis c
23	31	79.5	536	2 Q81897	Q81897 arabidopsis
24	31	79.5	627	2 Q7MRK6	Q7mrk6 porphyromon
25	31	79.5	1127	2 Q7YTU1	Q7ytu1 caenorhabdi
26	31	79.5	1161	2 Q8WQAO	Q8wqao caenorhabdi
27	31	79.5	1203	2 Q8S2E4	Q8s2e4 oryza sativ
28	31	79.5	1225	2 Q6GN12	Q6gn12 xenopus lae
29	31	79.5	1232	2 Q23998	Q23998 hordeum vul
30	31	79.5	1234	2 Q8GLU81	Q8glu81 cryza sativ
31	30	76.9	55	2 Q7SBT6	Q7sbt6 neurospora

32	30	76.9	213	2 Q9HX10	Q9hxl0 pseudomonas
33	30	76.9	226	2 Q8PDC5	Q8pdc5 xanthomonas
34	30	76.9	226	2 Q8PQ96	Q8pq96 xanthomonas
35	30	76.9	250	2 Q9ZUA5	Q9zuas arabidopsis
36	30	76.9	318	2 Q7Z8M2	Q7z8m2 emericella
37	30	76.9	318	2 AAQ07985	AAq07985 emericell
38	30	76.9	333	2 Q34933	Q34933 bacillus su
39	30	76.9	334	2 Q9XEN7	Q9xen7 triticum ae
40	30	76.9	401	2 Q6K489	Q6k489 oryza sativ
41	30	76.9	401	2 BAD19896	Bad19896 oryza sat
42	30	76.9	425	2 Q8RQO9	Q8rgg9 fusobacteri
43	30	76.9	686	2 Q9HCF9	Q9hcf9 homo sapien
44	30	76.9	708	2 Q7NIY1	Q7niy1 gloeobacter
45	30	76.9	737	2 Q8TBB6	Q8tbb6 homo sapien

ALIGNMENTS

RESULT 1

Q89EV1 PRELIMINARY; PRT; 153 AA.
AC Q89EV1
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Blr6969 protein.
GN OrderedLocusNames=blr6969;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
RN NCBI_TaxID=375;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110.
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko I., Nakamura Y., Sato S., Minamisawa K., Uchiuni T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsurucka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AF005960; SACS2234.1; -.
KW Complete proteome.
SQ SEQUENCE 153 AA; 15488 MW; 23C7D464AA94A490 CRC64;

Query Match 87.2%; Score 34; DB 2; Length 153;
Best Local Similarity 77.8%; Pred. No. 8.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
||| :|||
Db 73 GANAQAQLF 81

RESULT 2

Q6CIU3 PRELIMINARY; PRT; 130 AA.
AC Q6CIU3
DT 01-OCT-2004 (Tremblrel. 28, Created)
DT 01-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Similarity.
GN ORFNames=KLUAOF23936g;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
RN NCBI_TaxID=28985;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG GENOLEVURES;

RP SEQUENCE FROM N.A.

DR PROSITE; PS00027; HOMEBOX_1; FALSE_NEG.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nucleo protein; Repressor;

DR DR DR KTW

KW	Transcription regulation.
FT	DNA BIND 35 97 Homeobox; TALE-type.
SQ	SEQUENCE 269 AA; 29442 MW; 1074355DCCOC2253 CRC64;
	Query Match 84.68; Score 33; DB 1; Length 269;
	Best Local Similarity 77.88; Pred. No. 27;
	Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	1 GANAXSSLF 9
DB	222 GANAQSLG 230
	RESULT 5
LMP1_MOUSE	STANDARD; PRT; 406 AA.
ID	LMP1_MOUSE
AC	P11438; Q62020;
DT	01-OCT-1989 (Rel. 12, Created)
DT	01-AUG-1990 (Rel. 15, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (LGP-A)
DE	(LGP-120) (CD107A) (P2B).
GN	Name=Lamp1; Synonyms=Lamp-1;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=90307738; PubMed=2142158;
RA	Granger B.L., Green S.A., Gabel C.A., Howe C.L., Wellman I.,
RA	Helenius A.;
RT	"Characterization and cloning of lgp110, a lysosomal membrane
RT	glycoprotein from mouse and rat cells.";
RL	J. Biol. Chem. 265:12036-12043(1990).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Heffernan M., Yousefi S., Dennis J.W.;
RA	Submitted (FEB-1990) to the EMBL/GenBank/DDBJ databases.
RL	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6; TISSUE=Brain;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA	Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA	Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyar S.W.,
RA	Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[4]
RP	SEQUENCE OF 25-406 FROM N.A., AND PARTIAL SEQUENCE.
RP	MEDLINE=88243732; PubMed=3379044;
RX	Chen J.W., Cha Y., Yuksel K.U., Gracy R.W., August J.T.;
RT	"Isolation and sequencing of a cDNA clone encoding lysosomal membrane
RT	glycoprotein mouse LAMP-1. Sequence similarity to proteins bearing
RT	onco-differentiation antigens.";
RL	J. Biol. Chem. 263:8754-8758(1988).
RN	[5]
RP	DISULFIDE BONDS.
TX	MEDLINE=90237040; PubMed=2332434;
RA	Aterburn I.M., Earles B.J., August J.T.;
RT	"The disulfide structure of mouse lysosome-associated membrane protein
RT	1.";
RL	J. Biol. Chem. 265:7419-7423(1990).
CC	- FUNCTION: Presents carbohydrate ligands to selectins. Also
CC	implicated in tumor cell metastasis.
CC	- SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal. This
CC	protein shuttles between lysosomes, endosomes, and the plasma
CC	membrane.
CC	- PTM: O- and N-glycosylated; some of the N-glycans attached to
CC	LAMP-1 are polylactosaminoglycans [by similarity].
CC	- SIMILARITY: Belongs to the LAMP family.
CC	-----
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CC	-----
EMBL	N32015; AAA39428.1; .
DR	EMBL; M25244; AAA39869.1; .
DR	EMBL; BC049097; AAA49097.1; .
DR	EMBL; JO3881; AAA39411.1; .
DR	PIR; A28067; A28067.
DR	PIR; A60534; A60534.
DR	MGD; MG1:95745; Lamp1.
GO	GO:0005764; C:lysosome; IDA.
InterPro	IPRO02000; Lamp.
PRINTS	PR001299; Lamp; 1.
PRINTS	PR00336; LYSSASOCTDMP.
PROSITE	PS00310; LAMP_1; 2.
PROSITE	PS00311; LAMP_2; 1.
KW	Direct protein sequencing; Glycoprotein; Lysosome; Signal;
KW	Transmembrane. 1 24
FT	SIGNAL
FT	CHAIN 25 406
FT	-----
FT	1.
FT	Lysosome-associated membrane glycoprotein
FT	1.
FT	DOMAIN 25 370
FT	TRANSMEM 371 394
FT	DOMAIN 395 406
FT	DOMAIN 25 188
FT	DOMAIN 189 218
FT	DOMAIN 219 370
FT	DISULFD 35 74
FT	DISULFD 149 185
FT	DISULFD 222 259
FT	DISULFD 327 364
FT	CARBOHYD 31 31
FT	CARBOHYD 52 52
FT	CARBOHYD 58 58
FT	CARBOHYD 70 70
FT	CARBOHYD 78 78
FT	CARBOHYD 97 97
FT	CARBOHYD 101 101
FT	CARBOHYD 115 115
FT	CARBOHYD 159 159
FT	CARBOHYD 177 177
FT	CARBOHYD 214 214
FT	CARBOHYD 219 219
FT	CARBOHYD 232 232
FT	CARBOHYD 240 240

Wed Oct 27 09:38:10 2004

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Query Match      84.6%; Score 33; DB 1; Length 406;
Best Local Similarity 77.8%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GANAXSSLF 9
      |||||
DB      280 GMASSSLF 288

RESULT 6
Q8VH34 PRELIMINARY; PRT; 406 AA.
ID AC Q8VH34
DC Q8VH34; 2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE LAMP-1.
GN Name=Lamp1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ono K., Han J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY069968; AAL58070.1; -.
DR MGD; MGI:96745; Lamp1.
DR GO; GO:0005764; C:lysosome; IDA.
DR GO; GO:0005771; C:multivesicular body; IDA.
DR GO; GO:0042383; C:sarcolemma; IDA.
DR InterPro; IPR002000; Lamp.
DR Pfam; PF01299; Lamp; 1.
DR PRINTS; PR00336; LYSASSOCTDMP.
DR PROSITE; PS00310; LAMP 1; 2.
DR PROSITE; PS00311; LAMP 2; 1.
SQ SEQUENCE 406 AA; 43879 MW; C1BD373548ADFAB8 CRC64;

Query Match      84.6%; Score 33; DB 2; Length 406;
Best Local Similarity 77.8%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GANAXSSLF 9
      |||||
DB      280 GMASSSLF 288

RESULT 7
LMP1_RAT STANDARD; PRT; 407 AA.
ID LMP1_RAT
AC P14562; P97620;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (120
kDa lysosomal membrane glycoprotein) (LGP-120) (CD107A).
GN Name=Lamp1; Synonyms=LAMP-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Howe C.B., Granger B.L., Hull M., Green S.A., Gabel C.A., Helenius A.,
RA Mellman I.;
RT "Derived protein sequence, oligosaccharides, and membrane insertion of
the 120-kDa lysosomal membrane glycoprotein (lgp120): identification
of a highly conserved family of lysosomal membrane glycoproteins."
RL Proc. Natl. Acad. Sci. U.S.A. 85:7577-7581(1988).
RN [2]
RP SEQUENCE OF 22-407 FROM N.A.
RA MEDLINE=89153560; PubMed=2920835;
RX MEDLINE=89017240; PubMed=3174652;

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RA Himeno M., Noguchi Y., Sasaki H., Tanaka Y., Furuno K., Kono A.,
RA Sakaki Y., Kato K.;
RT "Isolation and sequencing of a cDNA clone encoding 107 kDa
RT sialoglycoprotein in rat liver lysosomal membranes."
RL FEBS Lett. 244:351-356(1989).
RN [3]
RP SEQUENCE OF 283-357 FROM N.A.
RC STRAIN=Wistar Kyoto; TISSUE=Aortic smooth muscle;
RA Adams L.A., Werny I., Schwartz S.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Presents carbohydrate ligands to selectins. Also
CC implicated in tumor cell metastasis.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal. This
CC protein shuttles between lysosomes, endosomes, and the plasma
CC membrane.
CC -!- PTM: O- and N-glycosylated; some of the N-glycans attached to
CC LAMP-1 are polylactosaminoglycans (by similarity).
CC -!- SIMILARITY: Belongs to the LAMP family.
CC -----
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CC -----
DR EMBL; M34959; AAA41525.1; -.
DR EMBL; X14765; CAA32873.1; -.
DR EMBL; U75406; AAB19108.1; -.
DR PIR; A30200; A30200.
DR GDI; 2989; Lamp1.
DR InterPro; IPR002000; Lamp.
DR Pfam; PF01299; Lamp; 1.
DR PRINTS; PR00336; LYSASSOCTDMP.
DR PROSITE; PS00310; LAMP 1; 2.
DR PROSITE; PS00311; LAMP 2; 1.
KW Glycoprotein; Lysosome; Signal; Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 407
FT Lysosome-associated membrane glycoprotein
FT 1.
FT Lumenal (Potential).
FT DOMAIN 22 371
FT TRANSMEM 372 395
FT DOMAIN 396 407
FT DOMAIN 22 189
FT DOMAIN 190 219
FT DOMAIN 220 371
FT DISULFID 36 75
FT DISULFID 150 186
FT DISULFID 223 260
FT DISULFID 328 365
FT CARBOHYD 32 32
FT CARBOHYD 59 59
FT CARBOHYD 71 71
FT CARBOHYD 79 79
FT CARBOHYD 102 102
FT CARBOHYD 116 116
FT CARBOHYD 123 125
FT CARBOHYD 145 145
FT CARBOHYD 160 160
FT CARBOHYD 178 178
FT CARBOHYD 215 215
FT CARBOHYD 220 220
FT CARBOHYD 223 233
FT CARBOHYD 241 241
FT CARBOHYD 271 271
FT CARBOHYD 283 283
FT CARBOHYD 297 297
FT CARBOHYD 312 312
FT CONFLICT 293 329
FT CONFLICT 329 329
FT CONFLICT 356 357
FT SEQUENCE 407 AA; 43969 MW; 25947490749A7C88 CRC64;
SQ

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Query Match		84.6%;	Score 33;	DB 1;	Length 407;				
Best Local Similarity		77.8%;	Pred. No. 43;						
Matches		7;	Conservative	0;	Mismatches				
				2;	Indels				
				0;	Gaps				
1 GANAXSSSLF 9									
QY									
DB	281 GGNATSSSLF 289								
RESULT 8									
Q9DC13 PRELIMINARY; PRT; 407 AA.									
AC	Q9DC13;								
DT	01-JUN-2001 (TRENBLrel. 17, Created)								
DT	01-JUN-2001 (TRENBLrel. 17, Last sequence update)								
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)								
DE	Mus musculus adult male lung cDNA, RIKEN full-length enriched library,								
DE	clone:1200007101 product:lysosomal membrane glycoprotein 1, full								
DE	insert sequence.								
GN	Name=Lamp1;								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=C57BL/6J; TISSUE=Lung;								
RX	MEDLINE=9279253; PubMed=10349636;								
RA	Carninci P., Hayashizaki Y.;								
RT	"High-efficiency full-length cDNA cloning.";								
RL	Meth. Enzymol. 303:19-44(1999).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=C57BL/6J; TISSUE=Lung;								
RX	MEDLINE=21085660; PubMed=11217851;								
RA	RIKEN FANTOM Consortium;								
RT	"Functional annotation of a full-length mouse cDNA collection.";								
RL	Nature 409:685-690(2001).								
RN	[3]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=C57BL/6J; TISSUE=Lung;								
RX	MEDLINE=20499374; PubMed=11042159;								
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,								
RA	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;								
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to								
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";								
RL	Genome Res. 10:1617-1630(2000).								
RN	[5]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=C57BL/6J; TISSUE=Lung;								
RX	MEDLINE=20530913; PubMed=11076861;								
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,								
RA	Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,								
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,								
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,								
RA	Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,								
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,								
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;								
RT	"RIKEN integrated sequence analysis (RISA) system-384-format								
RT	sequencing pipeline with 384 multicapillary sequencer.";								
RL	Genome Res. 10:1757-1771(2000).								
RN	[6]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=C57BL/6J; TISSUE=Lung;								
QY									
DB	281 GGNATSSSLF 289								
RESULT 9									
Q6D2C1 PRELIMINARY; PRT; 410 AA.									
ID	Q6D2C1;								
AC	Q6D2C1;								
DT	01-OCT-2004 (TRENBLrel. 28, Created)								
DT	01-OCT-2004 (TRENBLrel. 28, Last sequence update)								
DT	01-OCT-2004 (TRENBLrel. 28, Last annotation update)								
DE	Maltose-binding periplasmic protein.								
GN	Name=male; ORFNames=ECA3175;								
OS	Erwinia carotovora subsp. atroseptica SCRI11043.								
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;								
OC	Enterobacteriaceae; Pectobacterium.								
OX	NCBI_TaxID=218491;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=SCRI11043;								
RA	Bell K.S., Sebaihia M., Pritchard L., Holden M., Hyman L.J.,								
RA	Holeva M.C., Thomson N.R., Bentley S.D., Churcher C., Mungall K.,								
RA	Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,								
RA	Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,								
RA	Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,								
RA	Salmond G.P.C., Birch P.R.J., Barrrell B.G., Parkhill J., Toth I.K.;								
RL	Submitted (FEB-2004) to the ENBL/GenBank/DBJ databases.								
RL	EMBL; BX950851; CAG76073.1; -								
SQ	SEQUENCE 410 AA; 44608 MW; B2AD793237DE74F7 CRC64;								
Query Match						84.6%;	Score 33;	DB 2;	Length 410;
Best Local Similarity						77.8%;	Pred. No. 44;		
Matches						7;	Conservative	0;	Mismatches
								2;	Indels
								0;	Gaps
1 GANAXSSSLF 9									
QY									
DB	239 GANAIDSLF 247								
Query Match									
Best Local Similarity						84.6%;	Score 33;	DB 2;	Length 410;
Matches						7;	Conservative	0;	Mismatches
								2;	Indels
								0;	Gaps
1 GANAXSSSLF 9									
QY									
DB	239 GANAIDSLF 247								
Query Match									
Best Local Similarity						84.6%;	Score 33;	DB 2;	Length 410;
Matches						7;	Conservative	0;	Mismatches
								2;	Indels
								0;	Gaps
1 GANAXSSSLF 9									
QY									
DB	239 GANAIDSLF 24								

01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
 AgrD.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SA502A;
 RX MEDLINE=97342847; PubMed=9197262;
 RA Ji G., Beavis R., Novick R.P.;
 RT "Bacterial interference caused by autoinducing peptide variants."; Science 276:2027-2030(1997).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Gt31a-cp5, Gt31b-cp5, Gt36a-cp8, Gt36b-cp8, and Gt11-cp8;
 RC Goerke C., Dasbach S., Kuemmel M., Wolz C.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EXBL; AF001782; AB363265.1; -;
 DR EXBL; AJ617715; CAB22745.1; -;
 DR EXBL; AJ617716; CAB22748.1; -;
 DR EXBL; AJ617717; CAB22751.1; -;
 DR EXBL; AJ617718; CAB22754.1; -;
 DR EXBL; AJ617719; CAB22757.1; -;
 DR PIR; C89995; C89995.
 DR InterPro; IPR003229; AgrD.
 DR Pfam; PF05931; AgrD; 1.
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
 Query Match 82.1%; Score 32; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GANAXSSLF 9
 DB 24 GVNACSSLF 32
 RESULT 11
 QY 07A2N4 PRELIMINARY; PRT; 47 AA.
 AC Q7A2N4;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE AgrD protein.
 GN Name=agrD; OrderedLocusNames=SAV2037;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus."; Lancet 357:1225-1240(2001).
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003364; BAB58199.1; -;
 DR InterPro; IPR009229; AgrD.
 DR Pfam; PF05931; AgrD; 1.
 KW Complete proteome.
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
 Query Match 82.1%; Score 32; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GANAXSSLF 9
 DB 24 GVNACSSLF 32
 RESULT 11
 QY 07A2N4 PRELIMINARY; PRT; 47 AA.
 AC Q7A2N4;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE AgrD protein.
 GN Name=agrD; OrderedLocusNames=SAV2037;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus."; Lancet 357:1225-1240(2001).
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003364; BAB58199.1; -;
 DR InterPro; IPR009229; AgrD.
 DR Pfam; PF05931; AgrD; 1.
 KW Complete proteome.
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
 Query Match 82.1%; Score 32; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
 DB 24 GVNACSSLF 32
 RESULT 12
 QY 07A4I7 PRELIMINARY; PRT; 47 AA.
 AC Q7A4I7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE AgrD protein.
 GN Name=agrD; OrderedLocusNames=SA1842.1; ORFNames=SA5066;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus."; Lancet 357:1225-1240(2001).
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003364; BAB58199.1; -;
 DR InterPro; IPR009229; AgrD.
 DR Pfam; PF05931; AgrD; 1.
 KW Complete proteome.
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
 Query Match 82.1%; Score 32; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GANAXSSLF 9
 DB 24 GVNACSSLF 32
 RESULT 13
 QY 07A4I7 PRELIMINARY; PRT; 47 AA.
 AC Q7A4I7;
 DT 01-APR-2004 (TREMBlrel. 27, Created)
 DT 01-APR-2004 (TREMBlrel. 27, Last sequence update)
 DT 01-APR-2004 (TREMBlrel. 27, Last annotation update)
 DE AgrD protein.
 GN Name=agrD; OrderedLocusNames=SAV2037;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=gt31a-cp5;
 RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
 RT "Evolutionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococcus aureus."; Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ617715; CAB22745.1; -;
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
 Query Match 82.1%; Score 32; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GANAXSSLF 9

Db 24 GVNACSSLF 32

RESULT 14

CAE92748 PRELIMINARY; PRT; 47 AA.
 AC CAE92748; (TRENBLrel. 27, Created)
 DT 01-APR-2004 (TRENBLrel. 27, Last sequence update)
 DT 01-APR-2004 (TRENBLrel. 27, Last sequence update)
 DT 01-APR-2004 (TRENBLrel. 27, Last annotation update)
 DE AgrD protein.
 GN AGRD.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=gt31b-cp5;
 RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
 RT "Evolutionary Models for the Development of the Polymorphic Loci agr
 and cap in Staphylococcus aureus";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ617716; CAE92748.1; -
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 82.1%; Score 32; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
 Db 24 GVNACSSLF 32

RESULT 15

CAE92751 PRELIMINARY; PRT; 47 AA.
 AC CAE92751;
 DT 01-APR-2004 (TRENBLrel. 27, Created)
 DT 01-APR-2004 (TRENBLrel. 27, Last sequence update)
 DT 01-APR-2004 (TRENBLrel. 27, Last annotation update)
 DE AgrD protein.
 GN AGRD.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=gt33a-cp8;
 RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
 RT "Evolutionary Models for the Development of the Polymorphic Loci agr
 and cap in Staphylococcus aureus";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ617717; CAE92751.1; -
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 82.1%; Score 32; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GANAXSSLF 9
 Db 24 GVNACSSLF 32

Search completed: October 26, 2004, 16:04:56
 Job time : 42.6324 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:15 ; Search time 42.75 Seconds
(without alignments)
75.522 Million cell updates/sec

Title: US-10-032-950-3

Perfect score: 37

Sequence: 1 GVAAXSLP 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	94.6	9	3 AAY67853	Aay67853 S. aureus
2	35	94.6	9	5 AAM50901	Aam50901 AgrD-auto
3	35	94.6	9	5 ABP53542	Abp53542 Cyclic pe
4	31	83.8	163	5 ABU05504	Abu05504 M. tuberc
5	31	83.8	167	5 ABU05887	Abu05887 M. tuberc
6	31	83.8	167	6 ABP57498	Abp57498 Mycobacte
7	30	81.1	9	3 AAY67860	Aay67860 Staphyloc
8	30	81.1	9	3 AAY67859	Aay67859 Staphyloc
9	30	81.1	9	5 ABB07160	Abb07160 Peptide-m
10	30	81.1	9	5 AAM50907	Aam50907 Protected
11	30	81.1	9	5 AAM51004	Aam51004 AgrD2 lac
12	30	81.1	9	5 AAM51003	Aam51003 AgrD2 lin
13	30	81.1	9	5 AAM51002	Aam51002 AgrD2 lin
14	30	81.1	28	4 ABG15689	Abg15689 Novel hum
15	30	81.1	332	7 ABO83045	Abg83045 Pseudomon
16	30	81.1	347	7 ADC96234	Adc96234 E. faeciu
17	30	81.1	367	6 ABU29795	Abu29795 Protein e
18	30	81.1	543	2 AAY33146	Aay33146 Rabbit li
19	30	81.1	546	8 ADP87483	Adp87483 Rabbit li
20	30	81.1	564	8 ADP87485	Adp87485 Rabbit li
21	30	81.1	565	2 AAY33145	Aay33145 Rabbit li
22	30	81.1	565	8 ADG98216	Adg98216 Rabbit ca
23	30	81.1	566	3 AAB08202	Aab08202 Amino aci
24	30	81.1	2243	4 ABG29035	Abg29035 Novel hum
25	30	81.1	2478	4 ABG30281	Abg30281 Novel hum

26	29	78.4	9	3 AAY67851	Aay67851 S. aureus
27	29	78.4	9	3 AAY67861	Aay67861 Staphyloc
28	29	78.4	9	5 ABB07161	Abb07161 Peptide-m
29	29	78.4	9	5 AAM51005	Aam51005 AgrD2 lac
30	29	78.4	9	5 AAM50908	Aam50908 Protected
31	29	78.4	9	5 AAM50899	Aam50899 AgrD-auto
32	29	78.4	9	5 ABP53540	Abp53540 Cyclic pe
33	29	78.4	160	3 AAB19724	Aab19724 Human SEC
34	29	78.4	160	7 ADD18295	Add18295 Human mcl
35	29	78.4	161	3 AAB19725	Aab19725 Human SEC
36	29	78.4	161	7 ADD18297	Add18297 Human mol
37	29	78.4	272	4 ABG09243	Abg09243 Novel hum
38	28	75.7	9	2 AAB38323	Aab38323 Transcrip
39	28	75.7	9	5 ABB07159	Abb07159 Peptide-m
40	28	75.7	9	5 AAM51001	Aam51001 AgrD2 thi
41	28	75.7	9	6 ABB84631	Abb84631 S. aureus
42	28	75.7	9	7 ADF09190	Adf09190 S. aureus
43	28	75.7	9	8 ADJ98875	Adj98875 Peptide t
44	28	75.7	20	2 AAR37301	Aar37301 Rabbit Mu
45	28	75.7	31	3 AAB44017	Aab44017 Human can

ALIGNMENTS

RESULT 1

AAy67853

ID AAY67853 standard; peptide; 9 AA.

XX

AC AAY67853;

XX

DT 25-APR-2000 (first entry)

XX

DE S. aureus peptide #3 used for bacterial interference.

XX

KW Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;

KW virulence factor; treatment.

XX

OS Staphylococcus aureus.

XX

PH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal residue forms bond with C-terminal

FT residue to form a cyclic peptide"

FT Misc-difference 5

FT /label= Unknown

XX

PN WO9967286-A2.

XX

PD 29-DEC-1999.

 XX | PF | 24-JUN-1999; | 99WO-US014562. |

CC with this response in strains of different groups. The peptides and
 CC composition containing them can be used to treat infections by *S. aureus*
 XX
 SQ Sequence 9 AA;

Query Match 94.6%; Score 35; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVAAXSSLF 9
 |||||

Db 1 GVAAXSSLF 9

RESULT 2

AA050901

ID AA050901 standard; peptide; 9 AA.

XX

AC AA050901;

DT 08-MAY-2002 (first entry)

DE AgrD-autoinducing cyclic peptide, inhibitor of agr response.

XX Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
 KW antibacterial; infection; therapy; cyclic.

XX

OS Synthetic.

XX

FT Key Location/Qualifiers

FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"

FT Misc-difference 5 /note= "any amino acid"

FT Misc-difference 9 /note= "any amino acid"

FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"

XX

FN US6337385-B1.

XX

PD 08-JAN-2002.

XX

XX 24-JUN-1999; 99US-00339511.

XX

PR 24-JUN-1998; 98US-0090402P.

XX

PA (UTRQ) UNIV ROCKEFELLER.

XX

PA (UYN) UNIV NEW YORK STATE.

XX

PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX

DR WPI; 2002-170774/22.

XX

FT Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 FT interference and for treating Staphylococcus aureus infection in a
 FT subject.

XX

PS Claim 7; Col 19; 18pp; English.

XX

CC The present sequence is that of a novel synthetic cyclic peptide of the
 CC invention that is capable of inhibiting the agr response of
 CC Staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is
 CC a secreted agr-encoded peptide and where the agr locus controls the
 CC synthesis of virulence factor and other extracellular proteins
 CC responsible for pathogenicity in *S. aureus*. Preferred peptides may have
 CC the sequence NH₂-X(n)-2-X(y)-COOH, with a cyclic bond between the Z
 CC residue and COOH other than a thioester bond, where X is an amino acid,
 CC an amino acid analogue, a peptidomimetic or non-amide isoster, Z is a
 CC synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The
 CC cyclic bond is especially a lactam or lactone bond. The thiololactone
 CC structure within native AgrD peptides is required for activation of the
 CC agr response. Elimination of the thiol ester component of the cyclic ring
 CC structure can destroy agr response activating activity while preserving
 CC and enhancing inhibitory activity. A claimed method of preparing a cyclic

CC peptide involves: assembling a linear peptide chain on to a solid phase
 CC resin support; deprotecting the resulting protected assembled peptide;
 CC treating the deprotected peptide with neutral buffer for a time
 CC sufficient to form the cyclic peptide and cleave the peptide from the
 CC support; and recovering the cyclic peptide. The peptide is useful for
 CC bacterial interference, especially for the treatment of *S. aureus*
 CC infection

XX Sequence 9 AA;

Query Match 94.6%; Score 35; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVAAXSSLF 9
 |||||

Db 1 GVAAXSSLF 9

RESULT 3

ABP53542

ID ABP53542 standard; peptide; 9 AA.

XX

AC ABP53542;

XX

DT 13-DEC-2002 (first entry)

XX

DE Cyclic peptide SEQ ID NO:3.

XX

KW Cyclic peptide; Staphylococcus aureus; infection; antibacterial;

XX agr response inhibitor.

XX

OS Synthetic.

XX

FT Key Location/Qualifiers

FT Misc-difference 5 /note= "any amino acid"

FT

XX US2002077453-A1.

XX

PD 20-JUN-2002.

XX

XX 27-DEC-2001; 2001US-00032950.

XX

PR 24-JUN-1998; 98US-0090402P.

XX

PR 24-JUN-1999; 99US-00339511.

XX

PA (MUIR/) MUIR T W.

XX

PA (MAYV/) MAYVILLE P.

XX

PA (NOVI/) NOVICK R P.

XX

PA (BEAV/) BEAVIS R.

XX

PA (JIGG/) JI G.

XX

PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX

DR WPI; 2002-681366/73.

XX

PT New cyclic peptides, useful for treating Staphylococcus aureus

XX infections.

XX

PS Claim 9; Page 10; 18pp; English.

XX

CC ABP53540 to ABP53547 represent cyclic peptides (I) from the present

CC invention. The present invention also describes a method for treating

CC Staphylococcus aureus infection comprising the administration of a

CC composition comprising (I). (I) has antibacterial activity and can be

CC used as an agr gene response inhibitor. The peptides are useful for

CC treating *S. aureus* infections

XX

SQ Sequence 9 AA;

Query Match 94.6%; Score 35; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
 |||||
 Db 1 GVAAXSSLF 9

RESULT 4
 ABU05504
 ID ABU05504 standard; protein; 163 AA.
 XX AC ABU05504;
 XX DT 08-APR-2003 (first entry)
 XX DE M. tuberculosis and M. leprae marker protein #155.
 XX KW Mycobacterioses; survival; virulence; protective antigen; vaccine;
 XX KW Mycobacterial disease; tuberculosis; leprosy.
 XX OS Mycobacterium tuberculosis.
 XX OS Mycobacterium leprae.
 XX PN WO200274903-A2.
 XX PD 26-SEP-2002.
 XX PF 22-FEB-2002; 2002WO-IB001973.
 XX PR 22-FEB-2001; 2001US-0270123P.
 XX PA (INSP) INST PASTEUR.
 XX PI Cole S;
 XX DR WPI; 2002-759885/82.
 XX PT Identifying and selecting genes for survival or virulence of mycobacteria
 XX PT by a comparative genomic analysis of the sequences of Mycobacterium
 XX PT tuberculosis and M. leprae.
 XX FS Claim 17; Page 331; 874pp; English.
 XX CC This invention relates to a novel method for identifying essential genes
 XX CC for survival or virulence of mycobacteria species. The method comprises
 XX CC aligning the genomic sequence of a first mycobacterium species on a
 XX CC genomic sequence of a second mycobacterium species and selecting a
 XX CC polynucleotide sequence that is highly conserved in both genomes with no
 XX CC counterparts in other bacterial genomic sequences and that corresponds to
 XX CC an essential gene for the survival or virulence of mycobacterium species.
 XX CC The method of the invention is useful for detecting M. tuberculosis or M.
 XX CC leprae infection. The method reduces the number of potential new targets
 XX CC and protective antigens for new drugs and vaccine compositions to treat
 XX CC and prevent mycobacterial diseases, particularly tuberculosis and
 XX CC leprosy. The present sequence represents a marker protein from
 XX CC Mycobacterium tuberculosis and Mycobacterium leprae identified using the
 XX CC method of the invention
 XX SQ Sequence 163 AA;

Query Match 83.8%; Score 31; DB 5; Length 163;
 Best Local Similarity 77.8%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
 |||||
 Db 132 GVAASSAF 140

RESULT 5
 ABU05887
 ID ABU05887 standard; protein; 167 AA.
 XX AC ABU05887;
 XX DT 28-APR-2003 (first entry)
 XX DE Mycobacterium tuberculosis protein SEQ ID NO:125.
 XX KW Mycobacterium tuberculosis; infection; antibacterial; tuberculostatic;
 XX KW immunostimulant; vaccine; gene therapy; mycobacterial infection.
 XX OS Mycobacterium tuberculosis.
 XX OS

ABU05887;
 08-APR-2003 (first entry)
 M. tuberculosis and M. leprae marker protein #538.
 Mycobacterioses; survival; virulence; protective antigen; vaccine;
 mycobacterial disease; tuberculosis; leprosy.
 Mycobacterium tuberculosis.
 Mycobacterium leprae.
 WO200274903-A2.
 26-SEP-2002.
 22-FEB-2002; 2002WO-IB001973.
 22-FEB-2001; 2001US-0270123P.
 (INSP) INST PASTEUR.
 Cole S;
 WPI; 2002-759885/82.
 Identifying and selecting genes for survival or virulence of mycobacteria
 by a comparative genomic analysis of the sequences of Mycobacterium
 tuberculosis and M. leprae.
 Claim 17; Page 748; 874pp; English.
 This invention relates to a novel method for identifying essential genes
 for survival or virulence of mycobacteria species. The method comprises
 aligning the genomic sequence of a first mycobacterium species on a
 genomic sequence of a second mycobacterium species and selecting a
 polynucleotide sequence that is highly conserved in both genomes with no
 counterparts in other bacterial genomic sequences and that corresponds to
 an essential gene for the survival or virulence of mycobacterium species.
 The method of the invention is useful for detecting M. tuberculosis or M.
 leprae infection. The method reduces the number of potential new targets
 and protective antigens for new drugs and vaccine compositions to treat
 and prevent mycobacterial diseases, particularly tuberculosis and
 leprosy. The present sequence represents a marker protein from
 Mycobacterium tuberculosis and Mycobacterium leprae identified using the
 method of the invention
 Sequence 167 AA;

Query Match 83.8%; Score 31; DB 5; Length 167;
 Best Local Similarity 77.8%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
 |||||
 Db 136 GVAASSAF 144

RESULT 6
 ABP57498
 ID ABP57498 standard; protein; 167 AA.
 XX AC ABP57498;
 XX DT 28-APR-2003 (first entry)
 XX DE Mycobacterium tuberculosis protein SEQ ID NO:125.
 XX KW Mycobacterium tuberculosis; infection; antibacterial; tuberculostatic;
 XX KW immunostimulant; vaccine; gene therapy; mycobacterial infection.
 XX OS Mycobacterium tuberculosis.
 XX OS

PN WO2003000721-A2.
 XX 03-JAN-2003.
 XX 21-JUN-2002; 2002WO-GB002845.
 XX 22-JUN-2001; 2001GB-00015365.
 PR 07-SEP-2001; 2001GB-00021780.
 XX (MICR-) MICROBIOLOGICAL RES AUTHORITY.
 XX James BW, Bacon J, Marsh P;
 XX WPI; 2003-201403/19.
 DR N-PSDB; ABZ71124.
 XX New mycobacterial peptide, its fragment, variant or derivative, useful as
 PT vaccine for treating or preventing mycobacterial infections, and as
 PT diagnostic reagents for identifying such infections.
 XX
 PS Claim 2; Page 230; 246pp; English.
 XX ABP57436 to ABP57504 represent mycobacterial amino acid sequences (I)
 CC encoded by ABZ71062 to ABZ71130 (II), which are isolated from
 CC Mycobacterium tuberculosis. (I) are encoded by genes (II) whose
 CC expression is induced or up-regulated during culture of a mycobacterium
 CC under conditions defined by a dissolved oxygen tension of at least 10%
 CC air saturation measured at 37 plus degrees Celsius, when compared with a
 CC dissolved oxygen tension of at least 40% air saturation measured at 37
 CC plus degrees Celsius. (I) and (II) have antibacterial, tuberculostatic
 CC and immunostimulant activities, and can be used in vaccines and gene
 CC therapy. (I) and (II) can be used for the manufacture of a medicament for
 CC treating or preventing a mycobacterial infection. They can also be used
 CC for the manufacture of a diagnostic reagent for identifying a
 CC mycobacterial infection
 XX
 SQ Sequence 167 AA;
 Query Match 83.8%; Score 31; DB 6; Length 167;
 Best Local Similarity 77.8%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GVAAXSSSLF 9
 DB 136 GVAASSSAF 144
 RESULT 7
 AAY67860
 ID AAY67860 standard; peptide; 9 AA.
 AC AAY67860;
 XX 25-APR-2000 (first entry)
 XX Staphylococcus aureus AgrDII derived peptide sequence.
 XX Staphylococcus aureus infection; AgrD; agr response; treatment;
 KW virulence factor.
 XX Staphylococcus aureus.
 OS WO9967286-A2.
 PN 29-DEC-1999.
 PD 24-JUN-1999; 99WO-US014562.
 PF 24-JUN-1998; 98US-00103438.
 PR (UYRQ) UNIV ROCKEFELLER.
 PA (UYN) UNIV NEW YORK STATE.
 XX Muir TW, Mayville P, Novick RP, Ji G, Beavis R;
 XX WPI; 2000-147202/13.
 DR New cyclic peptides for treating infections with Staphylococcus aureus.
 PT Example; Page 22; 37pp; English.
 PS This sequence represents the Staphylococcus aureus AgrDII derived
 CC peptide. The invention relates to AgrD derived cyclic peptides, a
 CC composition containing a peptide and a carrier, and a method for the
 CC production of the cyclic peptides. The peptide inhibits the agr response,
 CC which is normally associated with the release of virulence factors of
 CC Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
 CC activates the agr response in strains of a single group, but interferes
 CC with this response in strains of different groups. The peptides and
 CC composition containing them can be used to treat infections by S. aureus
 XX

PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;
 XX WPI; 2000-147202/13.
 DR New cyclic peptides for treating infections with Staphylococcus aureus.
 PT Example; Page 22; 37pp; English.
 XX This sequence represents the Staphylococcus aureus AgrDII derived
 CC peptide. The invention relates to AgrD derived cyclic peptides, a
 CC composition containing a peptide and a carrier, and a method for the
 CC production of the cyclic peptides. The peptide inhibits the agr response,
 CC which is normally associated with the release of virulence factors of
 CC Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
 CC activates the agr response in strains of a single group, but interferes
 CC with this response in strains of different groups. The peptides and
 CC composition containing them can be used to treat infections by S. aureus
 XX
 SQ Sequence 9 AA;
 Query Match 81.1%; Score 30; DB 3; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GVAAXSSSLF 9
 DB 1 GVNASSSLF 9
 RESULT 8
 AAY67859
 ID AAY67859 standard; peptide; 9 AA.
 AC AAY67859;
 XX 25-APR-2000 (first entry)
 XX Staphylococcus aureus AgrDII derived peptide sequence.
 DE Staphylococcus aureus infection; treatment; AgrD; agr response;
 XX virulence factor.
 KW Staphylococcus aureus.
 OS WO9967286-A2.
 PN 29-DEC-1999.
 PD 24-JUN-1999; 99WO-US014562.
 PF 24-JUN-1998; 98US-00103438.
 PR (UYRQ) UNIV ROCKEFELLER.
 PA (UYN) UNIV NEW YORK STATE.
 XX Muir TW, Mayville P, Novick RP, Ji G, Beavis R;
 XX WPI; 2000-147202/13.
 DR New cyclic peptides for treating infections with Staphylococcus aureus.
 PT Example; Page 22; 37pp; English.
 PS This sequence represents the Staphylococcus aureus AgrDII derived
 CC peptide. The invention relates to AgrD derived cyclic peptides, a
 CC composition containing a peptide and a carrier, and a method for the
 CC production of the cyclic peptides. The peptide inhibits the agr response,
 CC which is normally associated with the release of virulence factors of
 CC Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
 CC activates the agr response in strains of a single group, but interferes
 CC with this response in strains of different groups. The peptides and
 CC composition containing them can be used to treat infections by S. aureus
 XX

Query Match 81.1%; Score 30; DB 5; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSSLF 9
 |||||
 Db 1 GVNASSSLF 9

RESULT 11

AAM51004
 ID AAM51004 standard; peptide; 9 AA.

XX AAM51004;

XX 07-AUG-2003 (revised)
 DT 08-MAY-2002 (first entry)

XX AgrD2 lactone cyclic peptide.

XX AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
 KW therapy; lactone; cyclic.

XX Staphylococcus aureus.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 5
 FT /note= "note linked to residue 9 to form cyclic peptide"
 FT Misc-difference 9

FT /note= "note linked to residue 5 to form cyclic peptide"
 XX US6337385-B1.

XX 08-JAN-2002.

XX 24-JUN-1999; 99US-00339511.

XX 24-JUN-1998; 98US-0090402P.

XX (UYRQ) UNIV ROCKEFELLER.

XX (UYN) UNIV NEW YORK STATE.

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX WPI; 2002-170774/22.

XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 PT interference and for treating Staphylococcus aureus infection in a
 PT subject.

XX Example 1; Col 9; 18pp; English.

XX The present sequence is that of a novel synthetic AgrD2 lactone cyclic
 CC peptide in which residue 5 of the peptide is linked to residue 9 via a
 CC lactone bond. The peptide is derived from an AgrD2 peptide of
 CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
 CC where the agr locus controls the synthesis of virulence factor and other
 CC extracellular proteins responsible for pathogenicity in *S. aureus*. The
 CC biological activity of the synthetic peptide was assayed using cultured
 CC *S. aureus* strains containing a beta-lactamase reporter gene fused to the
 CC agrP3 promoter. This allowed activation or inhibition of the agr response
 CC to be monitored spectrophotometrically. The lactone AgrD2 peptide
 CC inhibited the agr response of group I *S. aureus* strains without
 CC activating the agr response in group I, II or III strains. The invention
 CC provides claimed cyclic peptides (see AAM50899-906 and AAM50999) and
 CC methods for preparing them, especially peptides where the cyclic bond is
 CC a lactam or lactone bond. The cyclic peptides are useful for bacterial
 CC interference, especially for the treatment of *S. aureus* infection.
 CC (Updated on 07-AUG-2003 to correct OS field.)

XX Sequence 9 AA;

Query Match 81.1%; Score 30; DB 5; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSSLF 9
 |||||
 Db 1 GVNASSSLF 9

RESULT 12

AAM51003
 ID AAM51003 standard; peptide; 9 AA.

XX AAM51003;

XX 08-MAY-2002 (first entry)

XX AgrD2 linear free acid peptide.

XX AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
 KW therapy.

XX Staphylococcus aureus.
 OS Synthetic.

XX US6337385-B1.

XX 08-JAN-2002.

XX 24-JUN-1999; 99US-00339511.

XX 24-JUN-1998; 98US-0090402P.

XX (UYRQ) UNIV ROCKEFELLER.

XX (UYN) UNIV NEW YORK STATE.

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX WPI; 2002-170774/22.

XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 PT interference and for treating Staphylococcus aureus infection in a
 PT subject.

XX Example 1; Col 9; 18pp; English.

XX The present sequence is that of a novel synthetic AgrD2 linear free acid
 CC peptide. The peptide is derived from the cyclic AgrD2 peptide of
 CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
 CC where the agr locus controls the synthesis of virulence factor and other
 CC extracellular proteins responsible for pathogenicity in *S. aureus*. The
 CC biological activity of the synthetic peptide was assayed using cultured
 CC *S. aureus* strains containing a beta-lactamase reporter gene fused to the
 CC agrP3 promoter. This allowed activation or inhibition of the agr response
 CC to be monitored spectrophotometrically. Unlike an AgrD2 thiolactone
 CC cyclic peptide (see AAM51001), the present peptide was unable to either
 CC activate or inhibit the agr response, even when added to cultured cells
 CC at 10^6 concentrations. The invention provides claimed cyclic peptides (see
 CC AAM50899-906 and AAM50999) and methods for preparing them. The cyclic
 CC peptides are useful for bacterial interference, especially for the
 CC treatment of *S. aureus* infection

XX Sequence 9 AA;

Query Match 81.1%; Score 30; DB 5; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSSLF 9
 |||||
 Db 1 GVNASSSLF 9

DT 29-JUL-2004 (first entry)
 XX Pseudomonas aeruginosa polypeptide #15220.
 DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX
 KW Pseudomonas aeruginosa.
 XX OS
 XX US6551795-B1.
 XX PN
 XX 22-APR-2003.
 XX PD
 XX 18-FEB-1999; 99US-00252991.
 XX PF
 XX 18-FEB-1998; 98US-0074788P.
 XX PR
 XX 27-JUL-1998; 98US-0094190P.
 XX PR
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX PA
 XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX DR WPI; 2003-615309/58.
 XX DR N-PSDB; ABD16616.
 XX DR
 XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 XX PS Disclosure; SEQ ID NO 31791; 455pp; English.
 XX
 XX The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 XX SQ Sequence 332 AA;

Query Match 81.1%; Score 30; DB 7; Length 332;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVAAXSSLP 9
 | : | | | |
 Db 284 GIAATSMLF 292

Search completed: October 26, 2004, 15:59:41
 Job time : 43.75 secs

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:54:00 ; Search time 31.5 Seconds
(without alignments)
92.502 Million cell updates/sec

Title: US-10-032-950-3

Perfect score: 37

Sequence: 1 GVAAXSSLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	94.6	9	US-10-032-950-3	Sequence 3, Appli
2	32	86.5	391	US-10-156-761-9222	Sequence 9222, Ap
3	31	83.8	163	US-10-080-170-155	Sequence 155, App
4	31	83.8	163	US-10-080-170-155	Sequence 155, App
5	31	83.8	163	US-10-468-356-155	Sequence 155, App
6	31	83.8	167	US-10-080-170-538	Sequence 538, App
7	31	83.8	167	US-10-080-170-538	Sequence 538, App
8	31	83.8	167	US-10-468-356-538	Sequence 538, App
9	31	83.8	250	US-10-437-963-153774	Sequence 153774,
10	31	83.8	275	US-10-424-599-151015	Sequence 151015,
11	30	81.1	192	US-10-424-599-151015	Sequence 151015,
12	30	81.1	210	US-10-767-701-46362	Sequence 46362, A
13	30	81.1	367	US-10-767-701-37015	Sequence 37015, A
				US-10-282-122A-57719	Sequence 57719, A

14	30	81.1	565	14	US-10-267-756-2	Sequence 2, Appli
15	29	78.4	9	13	US-10-032-950-1	Sequence 1, Appli
16	29	78.4	50	15	US-10-424-599-151463	Sequence 151463,
17	29	78.4	140	16	US-10-437-963-146327	Sequence 146327,
18	29	78.4	150	16	US-10-767-701-37550	Sequence 37550, A
19	29	78.4	160	9	US-09-966-546-10	Sequence 10, Appl
20	29	78.4	160	9	US-09-966-545-10	Sequence 10, Appl
21	29	78.4	160	10	US-09-965-212-10	Sequence 10, Appl
22	29	78.4	160	14	US-10-189-940-10	Sequence 12, Appl
23	29	78.4	161	9	US-09-966-546-12	Sequence 12, Appl
24	29	78.4	161	9	US-09-966-545-12	Sequence 12, Appl
25	29	78.4	161	10	US-09-965-212-12	Sequence 12, Appl
26	29	78.4	161	14	US-10-189-940-12	Sequence 12, Appl
27	29	78.4	301	15	US-10-425-114-55553	Sequence 55553, A
28	29	78.4	658	16	US-10-437-963-185540	Sequence 185440,
29	29	78.4	841	16	US-10-437-963-138290	Sequence 138290,
30	29	78.4	1668	14	US-10-369-493-1181	Sequence 1181, Ap
31	28	75.7	9	14	US-10-201-444-3	Sequence 3, Appli
32	28	75.7	20	14	US-10-127-890-57	Sequence 57, Appl
33	28	75.7	31	9	US-09-925-301-1462	Sequence 1462, Ap
34	28	75.7	47	14	US-10-201-444-6	Sequence 6, Appli
35	28	75.7	55	15	US-10-424-599-242903	Sequence 242903,
36	28	75.7	58	15	US-10-424-599-214693	Sequence 214693,
37	28	75.7	132	15	US-10-425-114-54025	Sequence 54025, A
38	28	75.7	144	16	US-10-767-701-35453	Sequence 35453, A
39	28	75.7	153	15	US-10-284-049-3838	Sequence 3838, Ap
40	28	75.7	185	15	US-10-425-114-46475	Sequence 46475, A
41	28	75.7	282	15	US-10-425-114-59515	Sequence 59515, A
42	28	75.7	290	15	US-10-425-114-53919	Sequence 53919, A
43	28	75.7	305	16	US-10-437-963-193017	Sequence 193017,
44	28	75.7	364	10	US-09-919-039-343	Sequence 343, App
45	28	75.7	364	14	US-10-205-219-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1

US-10-032-950-3
; Sequence 3, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-3

Query Match 94.6%; Score 35; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cv 1 GVAAXSSLF 9

```

Db      1 GVAAXSLF 9
|||||||
RESULT 2
US-10-156-761-9222
; Sequence 9222, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-282
; CURRENT APPLICATION NUMBER: US/10/156.761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9222
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9222

Query Match      86.5%; Score 32; DB 14; Length 391;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GVAAXSLF 9
|||||||
Db      274 GVAAXSLF 282
|||||||
RESULT 3
US-10-080-170-155
; Sequence 155, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080.170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-080-170-155

Query Match      83.8%; Score 31; DB 14; Length 163;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GVAAXSLF 9
|||||||
Db      132 GVAAXSLF 140
|||||||
RESULT 4
US-10-080-170-155
; Sequence 155, Application US/10468356
; Publication No. US20040197896A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 05394.0019
; CURRENT APPLICATION NUMBER: US/10/468.356
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 10/080,170
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 655
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 155
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-468-356-155

Query Match      83.8%; Score 31; DB 17; Length 163;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GVAAXSLF 9
|||||||
Db      132 GVAAXSLF 140
|||||||
RESULT 5
US-10-468-356-155
; Sequence 155, Application US/10468356
; Publication No. US20040197896A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 05394.0019
; CURRENT APPLICATION NUMBER: US/10/468.356
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 10/080,170
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 655
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 155
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-468-356-155

Query Match      83.8%; Score 31; DB 17; Length 163;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GVAAXSLF 9
|||||||
Db      132 GVAAXSLF 140
|||||||
RESULT 6
US-10-080-170-538
; Sequence 538, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080.170

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; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-538

Query Match      83.8%; Score 31; DB 14; Length 167;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSSLF 9
Db 136 GVAASSAF 144

RESULT 7
US-10-080-170-538
; Sequence 538, Application US/10080170
; Publication No. US20040121322A9
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-538

Query Match      83.8%; Score 31; DB 16; Length 167;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSSLF 9
Db 136 GVAASSAF 144

US-10-468-356-538
; Sequence 538, Application US/10468356
; Publication No. US20040197896A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 05394.0019
; CURRENT APPLICATION NUMBER: US/10/468,356
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 10/080,170
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 655
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 538
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis

US-10-424-599-151015
; Sequence 151015, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 151015
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(275)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_107390C.1.pap
US-10-424-599-151015
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Query Match 83.8%; Score 31; DB 15; Length 275;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSLF 9
||| |||
Db 28 GVAESSLF 36

RESULT 11
US-10-767-701-46362
; Sequence 46362, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46362
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C17501_1.pep
US-10-767-701-46362

Query Match 81.1%; Score 30; DB 16; Length 192;
Best Local Similarity 87.5%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVAAXSSL 8
||| |||
Db 123 GVAAXSSL 130

RESULT 12
US-10-767-701-37015
; Sequence 37015, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 37015
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C13715_1.pep
US-10-767-701-37015

Query Match 81.1%; Score 30; DB 16; Length 210;
Best Local Similarity 77.8%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSLF 9
||| |||
Db 142 GVAATSLF 150

RESULT 13

US-10-282-122A-57719
; Sequence 57719, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malore, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 57719
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (32)..(32)
; OTHER INFORMATION: X=any amino acid
US-10-282-122A-57719

Query Match 81.1%; Score 30; DB 15; Length 367;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSLF 9
||| |||
Db 119 GVAAGSIF 127

RESULT 14
US-10-267-756-2
; Sequence 2, Application US/10267756
; Publication No. US20030235811A1
; GENERAL INFORMATION:
; APPLICANT: Redinbo, Matthew
; APPLICANT: Sompop, Bencharit
; APPLICANT: Potter, Philip
; APPLICANT: Morton, Christopher
; TITLE OF INVENTION: CRYSTALLIZED MAMMALIAN CARBOXYLESTERASE POLYPEPTIDE AND SCREENING
; TITLE OF INVENTION: EMPLOYING SAME

; FILE REFERENCE: Attorney Docket No. US20030235811A1 421-63-2
; CURRENT APPLICATION NUMBER: US/10/267,756
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/374,513
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 565
; TYPE: PPT
; ORGANISM: Oryctolagus cuniculus
US-10-267-756-2

Query Match 81.1%; Score 30; DB 14; Length 565;
Best Local Similarity 77.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVAAXSLF 9
Db 248 GVALLSLF 256

RESULT 15

US-10-032-950-1
; Sequence 1, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-1

Query Match 78.4%; Score 29; DB 13; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVAAXSLF 9
Db 1 GVNAXSLF 9

Search completed: October 26, 2004, 16:10:11
Job time : 32.5 secs

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:46:55 ; Search time 8.73529 Seconds
(without alignments)
99.132 Million cell updates/sec

Title: US-10-032-950-3
Perfect score: 37
Sequence: 1 GVAAXSSLF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	89.2	1253	2 T18528	probable pyruvate
2	31	83.8	163	2 A87066	conserved hypothet
3	31	83.8	167	2 C70866	hypothetical prote
4	31	83.8	169	2 T45243	hypothetical prote
5	30	81.1	244	2 A40049	virC-region lipopr
6	30	81.1	244	2 T43566	translocation lipo
7	30	81.1	267	2 B83602	conserved hypothet
8	30	81.1	305	2 AC2730	probable integral
9	30	81.1	305	2 D97511	carboxylesterase (
10	30	81.1	539	2 A29923	hypothetical prote
11	29	78.4	367	2 B64399	hypothetical prote
12	29	78.4	398	2 F85056	hypothetical prote
13	29	78.4	1668	1 C69224	cobalamin biosynth
14	28	75.7	42	2 I51291	aldolase C - chick
15	28	75.7	47	2 C89995	AgrD protein (limp
16	28	75.7	282	2 T15556	hypothetical prote
17	28	75.7	330	2 D82756	pyridoxal phosphat
18	28	75.7	331	2 S33223	transcription fact
19	28	75.7	338	1 Q85204	sfuA protein precu
20	28	75.7	338	2 T43918	probable iron-bind
21	28	75.7	339	2 AH0359	iron(III)-binding
22	28	75.7	348	2 T12291	NADH2 dehydrogenas
23	28	75.7	348	2 T12290	NADH2 dehydrogenas
24	28	75.7	363	1 ADREA	fructose-bisphosph
25	28	75.7	364	1 ADHUA	fructose-bisphosph
26	28	75.7	364	1 ADMSA	fructose-bisphosph
27	28	75.7	364	1 ADRTA	fructose-bisphosph
28	28	75.7	382	2 S33630	ADP/ATP carrier pr
29	28	75.7	386	2 S17917	ADP/ATP carrier pr

30	28	75.7	386	2 S21974	ADP/ATP carrier pr
31	28	75.7	387	2 S16568	ADP/ATP carrier pr
32	28	75.7	387	2 S14876	ADP/ATP carrier pr
33	28	75.7	396	2 AH2859	MFS permease (limp
34	28	75.7	396	2 F97636	probable transport
35	28	75.7	442	2 AF2539	manganese transpor
36	28	75.7	523	2 T07834	hydroxymethylpyrim
37	28	75.7	525	2 E86363	probable thiamin b
38	28	75.7	549	2 T23422	hypothetical prote
39	28	75.7	612	2 T23420	hypothetical prote
40	28	75.7	639	2 T23424	hypothetical prote
41	28	75.7	981	2 B88794	protein K07F5.12a
42	27	73.0	182	2 AB1251	hypothetical prote
43	27	73.0	184	2 T46711	hypothetical prote
44	27	73.0	188	2 B38116	hypothetical prote
45	27	73.0	188	2 AC2563	transposase air850

ALIGNMENTS

RESULT 1

T18528
Probable pyruvate (flavodoxin) dehydrogenase (EC 1.2.99.-) - Giardia intestinalis
N;Alternate names: pyruvate:ferredoxin oxidoreductase
C;Species: Giardia intestinalis
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T18528

R;Townson, S.M.; Hanson, G.R.; Upcroft, J.A.; Upcroft, P.
Eur. J. Biochem. 220, 439-446, 1994
A;Title: A purified ferredoxin from Giardia duodenalis.
A;Reference number: S42359; MUID:94170792; PMID:8125101
A;Accession: T18528
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1253 <TOW>
A;Cross-references: UNIPROT:Q24982; EMBL:I27221; NID:G960281; PID:G960283; PIDN:AAA7489
C;Function:

A;Description: may be involved in electron transfer from pyruvate to flavodoxin
C;Superfamily: pyruvate (flavodoxin) dehydrogenase; ferredoxin 2[4Fe-4S] homology
C;Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein; oxidoreduct

Query Match 89.2%; Score 33; DB 2; Length 1253;

Best Local Similarity 77.8%; Pred. No. 19;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVAAXSSLF 9

Db 906 GIAACSSLF 914

RESULT 2

A87066
conserved hypothetical protein ML1255 [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C;Accession: A87066

R;Cole, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H.
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S

A;Title: Massive gene decay in the leprosy bacillus

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: A87066

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-163 <STO>

A;Cross-references: UNIPROT:Q9CC58; GB:AL450380; NID:G13093193; PIDN:CAC31636.1; GSPDB:

C;Genetics: ML1255

C;Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16

Query Match 83.8%; Score 31; DB 2; Length 163;
 Best Local Similarity 77.8%; Pred. No. 7.7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSSSLF 9
 |||||
 DB 132 GVAASASAF 140

RESULT 3
 C70866
 hypothetical protein RV2468c - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: C70866
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: C70866
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-167 <COL>
 A:Cross-references: UNIPROT:O53195; GB:AL021246; GB:AL123456; NID:g3261507; PIDN:CAA1604
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV2468c
 C:Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16

Query Match 83.8%; Score 31; DB 2; Length 167;
 Best Local Similarity 77.8%; Pred. No. 7.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSSSLF 9
 |||||
 DB 136 GVAASASAF 144

RESULT 4
 T45243
 hypothetical protein MLCB1610.16 [imported] - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T45243
 R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, March 1999
 A:Reference number: 222949
 A:Accession: T45243
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-169 <JAM>
 A:Cross-references: UNIPROT:Q9X7B5; EMBL:AL049913; PIDN:CAB43162.1
 A:Experimental source: cosmid B1610
 C:Genetics:
 A:Note: MLCB1610.16
 C:Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16

Query Match 83.8%; Score 31; DB 2; Length 169;
 Best Local Similarity 77.8%; Pred. No. 7.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSSSLF 9
 |||||
 DB 138 GVAASASAF 146

RESULT 5
 A40049
 virC-region lipoprotein yscJ (vlpB) - Yersinia enterocolitica plasmid pVY
 C:Species: Yersinia enterocolitica

Query Match 81.1%; Score 30; DB 2; Length 244;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVAAXSSSLF 9
 |||||
 DB 143 GVAASASAF 151

RESULT 7
 B83602
 conserved hypothetical protein PA0340 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: B83602
 R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

C:Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 09-Jul-2004
 C:Accession: A40049
 R:Michiels, T.; Vanooteghem, J.C.; Lambert de Rouvroit, C.; China, B.; Gustin, A.; Boudt, J. Bacteriol. 173, 4994-5009, 1991
 A:Title: Analysis of virC, an operon involved in the secretion of Yop proteins by Yersinia
 A:Reference number: A40361; MUID:91317716; PMID:1860816
 C:Accession: A40049
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-244 <MIC>
 A:Cross-references: UNIPROT:Q01251; GB:M74011; NID:g155549; PIDN:AAC37027.1; PID:g155559
 C:Genetics:
 A:Genome: plasmid
 C:Superfamily: invasin secretion factor mxjJ
 C:Keywords: lipid binding; lipoprotein

Query Match 81.1%; Score 30; DB 2; Length 244;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVAAXSSSLF 9
 |||||
 DB 143 GVAASASAF 151

RESULT 6
 T43566
 translocation lipoprotein J - Yersinia pestis plasmid pCD1
 C:Species: Yersinia pestis
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T43566; T42861
 R:Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker, J. Bacteriol. 180, 5192-5202, 1998
 A:Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
 A:Reference number: 222578; MUID:98422474; PMID:9748454
 A:Accession: T43566
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-244 <HUP>
 A:Cross-references: UNIPROT:Q00926; EMBL:AF053946; NID:g2996222; PIDN:AAC62607.1; PID:g2996222
 A:Experimental source: strain KIM
 R:Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. Infect. Immun. 66, 4611-4623, 1998
 A:Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia P
 A:Reference number: 222273; MUID:98427122; PMID:9746557
 A:Accession: T42861
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-244 <PER>
 A:Cross-references: EMBL:AF074612; NID:g3822037; PIDN:AAC69775.1; PID:g3822055
 A:Experimental source: strain KIM5
 C:Genetics:
 A:Gene: yscJ
 A:Genome: plasmid pCD1
 C:Superfamily: invasin secretion factor mxjJ

Query Match 81.1%; Score 30; DB 2; Length 244;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVAAXSSSLF 9
 |||||
 DB 143 GVAASASAF 151

```

.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B93602
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <STO>
A;Cross-references: UNIPROT:Q916F3; GB:AB004472; GB:AB004091; NID:g9946188; PIDN:AA0372
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0340
C;Superfamily: hypothetical protein HI0902

Query Match      81.1%; Score 30; DB 2; Length 267;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSSLF 9
Db 219 GIAATSLMF 227

RESULT 8
AC2730
conserved hypothetical protein Atul248 [imported] - Agrobacterium tumefaciens (strain. C5
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AC2730
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC2730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-305 <KUR>
A;Cross-references: UNIPROT:Q8UFZ6; GB:AB008688; PIDN:AAU42257.1; PID:g17739654; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul248
A;Map position: circular chromosome

Query Match      81.1%; Score 30; DB 2; Length 305;
Best Local Similarity 87.5%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAAXSSLF 9
Db 127 VAATSSLF 134

RESULT 9
D97511
probable integral membrane protein. (AL132674) [imported] - Agrobacterium tumefaciens (s
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97511
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D97511
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-305 <KUR>
A;Cross-references: UNIPROT:Q8UFZ6; GB:AB007869; PIDN:AAK67045.1; PID:g15156295; GSPDB:G
C;Genetics:

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A;Gene: AGR_C_2304
A;Map position: circular chromosome

Query Match      81.1%; Score 30; DB 2; Length 305;
Best Local Similarity 87.5%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VAAXSSLF 9
Db 127 VAATSSLF 134

RESULT 10
A29923
carboxylesterase (EC 3.1.1.1), TCCD-induced 60K microsomal - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 08-Dec-1988 #sequence_revision 08-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29923; A29471
R;Korza, G.; Ozols, J.
J. Biol. Chem. 263, 3486-3495, 1988
A;Title: Complete covalent structure of 60-kDa esterase isolated from 2,3,7,8-tetrachloro
A;Reference number: A29923; MUID:88139431; PMID:3343253
A;Accession: A29923
A;Molecule type: protein
A;Residues: 1-539 <KOR>
A;Cross-references: UNIPROT:P12337
R;Ozols, J.
J. Biol. Chem. 262, 15316-15321, 1987
A;Title: Isolation and characterization of a 60-kilodalton glycoprotein esterase from 1:
A;Reference number: A29471; MUID:88033124; PMID:3667634
A;Accession: A29471
A;Molecule type: protein
A;Residues: 1-71; 193-208; 436-446; 532-539 <OZO>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein
F;32-526/Domain: cholinesterase homology <CHE>
F;61.363/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;195.441/Active site: Ser, His #status experimental

Query Match      81.1%; Score 30; DB 2; Length 539;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVAAXSSLF 9
Db 222 GVALLSLF 230

RESULT 11
E64399
hypothetical protein MJ0797 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: E64399
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi
A;Reference number: A84300; MUID:96337999; PMID:8688087
A;Accession: E64399
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-367 <BUL>
A;Cross-references: UNIPROT:Q58207; GB:U67524; GB:L77117; NID:g2826321; PIDN:AA098792.1
C;Genetics:
A;Map position: FOR720661-721764

Query Match      78.4%; Score 29; DB 2; Length 367;
Best Local Similarity 87.5%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GVAAXSSL 8
Db      27 GVAAISSL 34
|||||
|

RESULT 12
F85056
Hypothetical protein AT904480 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (musc-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F85056
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: F85056
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-398 <STO>
A:Cross-references: UNIPROT:Q9XEC5; GB:NC_001268; NID:g7267205; PIDN:CAB77916.1; GSPDB:G
C:Genetics:
A:Gene: AT904480
A:Map position: 4

Query Match      78.4%; Score 29; DB 2; Length 398;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GVAAXSSLF 9
Db      289 GVSASVSF 297
|||||
|

RESULT 13
C69224
cobalamin biosynthesis protein N - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: C69224
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A>Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcn
A:Reference number: A69000; MUID:98037514; PMID:93711463
A:Accession: C69224
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1668 <MTH>
A:Cross-references: UNIPROT:O27011; GB:AF000066; NID:g2622025; PIDN:AAB8542
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH928
A:Start codon: GTG
C:Superfamily: Methanobacterium thermoautotrophicum cobalamin biosynthesis protein N

Query Match      78.4%; Score 29; DB 1; Length 1668;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GVAAXSSLF 9
Db      1273 GIAAISLRF 1281
|||||
|

RESULT 14
I51291
aldolase C - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C:Accession: I51291
R:Meighan-Mantha, R.L.; Tolan, D.R.
J. Cell. Biochem. 57, 423-431, 1995

```

A>Title: Noncoordinate changes in the steady-state mRNA expressed from aldolase A and al

A:Reference number: I51291; MUID:95286677; PMID:7768978

A:Accession: I51291

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-42 <MEI>

A:Cross-references: UNIPROT:Q92007; GB:S78288; NID:g999389; PIDN:AAB34479.1; PID:g999390

C:Superfamily: fructose-bisphosphate aldolase

Query Match 75.7%; Score 28; DB 2; Length 42;

Best Local Similarity 66.7%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9

Db 28 GAAASESLF 36

|||||

||

RESULT 15

C89995

Agd protein [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: C89995

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: C89995

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-47 <KUR>

A:Cross-references: UNIPROT:O33586; GB:BA000018; PID:gl3701831; PIDN:BA843124.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: agrD

Query Match 75.7%; Score 28; DB 2; Length 47;

Best Local Similarity 77.8%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9

Db 24 GWNACSSLF 32

|||||

||

Search completed: October 26, 2004, 16:06:07

Job time : 9.73529 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:50 ; Search time 40.6324 Seconds
(without alignments)
127.445 Million cell updates/sec

Title: US-10-032-950-3

Perfect score: 37

Sequence: 1 GVAAXSSLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	91.9	377	Q8L676	Oryza sativ
2	33	89.2	1087	Q7QZK4	Q7qzK4 giardia lam
3	33	89.2	1253	Q24982	Q24982 giardia lam
4	32	86.5	385	Q8SRV6	Q8sry6 encephalito
5	32	86.5	391	Q82NH7	Q82nh7 streptomyc
6	32	86.5	788	Q7SDP5	Q7sd5 neurospora
7	32	86.5	1289	Q7PZ77	Q7pz77 anopheles g
8	31	83.8	158	Q73XW1	Q73xm1 mycobacteri
9	31	83.8	158	AAS04605	Aas04605 mycobacte
10	31	83.8	163	Q9CC58	Q9cc58 mycobacteri
11	31	83.8	167	Q53195	Q53195 mycobacteri
12	31	83.8	167	Q7TVI6	Q7tyi6 mycobacteri
13	31	83.8	169	Q9X7B5	Q9x7b5 mycobacteri
14	31	83.8	255	Q9LZ76	Q9lz76 oryza sativ
15	30	81.1	191	Q6K371	Q6kb71 sorghum bic
16	30	81.1	191	CAG30668	Cag30668 sorghum b
17	30	81.1	236	Q56969	Q56969 versinia pe
18	30	81.1	244	1 YSCJ YEREN	O01251 versinia en
19	30	81.1	244	1 YSCJ YERPE	O00926 versinia pe
20	30	81.1	244	AAK69242	Aak69242 versinia
21	30	81.1	244	AAK16843	Aak16843 versinia
22	30	81.1	244	AAN37545	Aan37545 versinia
23	30	81.1	260	Q7U5Z1	Q7u5z1 synchococc
24	30	81.1	267	Q916F3	Q916f3 pseudomonas
25	30	81.1	305	Q7CZN5	Q7czn5 agrobacteri
26	30	81.1	305	Q8UFZ6	Q8ufz6 agrobacteri
27	30	81.1	398	Q7NPK4	Q7npk4 Gloebacter
28	30	81.1	565	EST1_RABIT	F12337 cryptolagus
29	30	81.1	578	Q7P548	Q7p548 fusobacteri
30	30	81.1	586	Q6BH24	Q6bh24 debaryomyce
31	29	78.4	97	Q7S8M4	Q7s8m4 neurospora

32 29 78.4 163 2 Q836B5
33 29 78.4 281 2 Q7ULX9
34 29 78.4 298 2 Q8SVA3
35 29 78.4 302 2 Q87JD9
36 29 78.4 335 2 Q88G45
37 29 78.4 352 2 Q7MQZ7
38 29 78.4 367 1 Y797.METJA
39 29 78.4 388 2 Q8N4S1
40 29 78.4 398 2 Q9XEC5
41 29 78.4 403 2 Q9HKZ8
42 29 78.4 418 2 Q979S9
43 29 78.4 522 2 Q7MSA0
44 29 78.4 524 2 Q7KRA2
45 29 78.4 524 2 AAS64847

ALIGNMENTS

RESULT 1

Q8L676 PRELIMINARY; PRT; 377 AA.
AC Q8L676;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein OSJNB0011109.21.
GN ORFNames=OSJNB0011109.21;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Teitron T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feldblum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RL The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
chromosome 10.";
RL Science 300:1566-1569 (2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wang R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092388; AAM22720.1; -;
DR EMBL; AB017090; AAP53582.1; -;
DR Gramene; Q8L676; -;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M:esterase.
DR InterPro; IPR006186; T:phatase apah.
DR Pfam; PF00149; Metallophos; 1_
DR ProDom; PD000252; T:phatase_apah; 1.
KW Hypothetical protein.
SQ SEQUENCE 377 AA; 40656 MW; C18C31695D85B459 CRC64;

Query Match 91.9%; Score 34; DB 2; Length 377;

Best Local Similarity 77.8%; Pred. No. 22;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVAAXSSLF 9

DB 239 GVAAXSSLF 247

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RESULT 2
Q70ZK4 PRELIMINARY; PRT; 1087 AA.
AC Q70ZK4; 2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 159 16450 19713.
OS Giardia_lambliA ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AACB01000042; EAA40460.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR005479; Cphp_synth_L_D2.
DR InterPro; IPR002869; POR.
DR InterPro; IPR002880; POR.N.
DR InterPro; IPR000399; Pyruvate decarb.
DR Pfam; PF00037; Fer4; 2.
DR Pfam; PF01559; POR; 1.
DR Pfam; PF01855; POR.N; 1.
DR Pfam; PF02775; TPP enzyme C; 1.
DR PRINTS; PR00353; 4FE4SPRDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN 1.
KW 4Fe-4S; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 1087 AA; 121060 MW; ASB172F5A56419C9 CRC64;
Preliminary data.
Query Match 89.2%; Score 33; DB 2; Length 1087;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
Db 740 GIAACSLF.748

RESULT 3
Q24982 PRELIMINARY; PRT; 1253 AA.
AC Q24982;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pyruvate:ferredoxin oxidoreductase.
OS Giardia_lambliA (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94170792; PubMed=8125101;
RA Townson S.M., Hanson G.R., Upcroft J.A., Upcroft P.;
RT "A purified ferredoxin from Giardia duodenalis.";
RL Eur. J. Biochem. 220:439-446(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Upcroft P., Healey A., Upcroft J., Townson S.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

Query Match 89.2%; Score 33; DB 2; Length 1087;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
Db 740 GIAACSLF.748

RESULT 4
Q8SRY6 PRELIMINARY; PRT; 385 AA.
AC Q8SRY6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative AMINOACID TRANSPORTER.
GN Name=ECU05_0580;
OS Encephalitozoon cuniculi.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL590445; CAD26577.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR Pfam; PF01490; Aa trans; 1.
DR Pfam; PF01490; Aa trans; 1.
SQ SEQUENCE 385 AA; 43605 MW; 0EEB01706C82ECAE CRC64;
Query Match 85.5%; Score 32; DB 2; Length 385;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9

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DR EMBL; L27221; AAA74894.1; -.
DR PIR; T18528; T18528.
DR HSP; P94692; 1KEK.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR002869; POR.
DR InterPro; IPR002880; POR.N.
DR InterPro; IPR000399; Pyruvate decarb.
DR InterPro; IPR009014; Transketo_C_like.
DR Pfam; PF00037; Fer4; 2.
DR Pfam; PF01558; POR; 1.
DR Pfam; PF01855; POR.N; 1.
DR Pfam; PF02775; TPP enzyme C; 1.
DR PRINTS; PR00353; 4FE4SPRDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN 1.
KW 4Fe-4S; Iron; Iron-sulfur; Metal-binding; Pyruvate.
SQ SEQUENCE 1253 AA; 138928 MW; FF3B74820DEA8B21 CRC64;
Query Match 89.2%; Score 33; DB 2; Length 1253;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
Db 906 GIAACSLF.914

RESULT 4
Q8SRY6 PRELIMINARY; PRT; 385 AA.
AC Q8SRY6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative AMINOACID TRANSPORTER.
GN Name=ECU05_0580;
OS Encephalitozoon cuniculi.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL590445; CAD26577.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR Pfam; PF01490; Aa trans; 1.
DR Pfam; PF01490; Aa trans; 1.
SQ SEQUENCE 385 AA; 43605 MW; 0EEB01706C82ECAE CRC64;
Query Match 85.5%; Score 32; DB 2; Length 385;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9

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Db      374 GVAFAASLF 382
||||:||||
Q82MH7 PRELIMINARY; PRT; 391 AA.
RESULT 5
ID Q82MH7 PRELIMINARY; PRT; 391 AA.
AC Q82MH7; 24, Created
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=SAV1683;
OS Streptomyces avermitilis;
OC Bacteria; Actinobacteria; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VA-4680;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005027; BAC69394.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 391 AA; 42006 MW; B3BD8F2F27CAE3D8 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 391;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
||||:||||
Db 274 GVAASVSLF 282

RESULT 6
Q7SDF5 PRELIMINARY; PRT; 788 AA.
AC Q7SDF5; 26, Created
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Predicted protein.
DE Name=NCU09316.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Tanakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenkoff C.P., Kinsey J.A., Braun E.D., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

RA Kamal M., Kamvysselis M., Mauceli E., Bielek C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osman S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX0100055; EAA34784.1; -
SQ SEQUENCE 788 AA; 83602 MW; FE558C3E25E31E5A CRC64;

Query Match 86.5%; Score 32; DB 2; Length 788;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
||||:||||
Db 61 GTATSSLF 69

RESULT 7
Q7PZ77 PRELIMINARY; PRT; 1289 AA.
AC Q7PZ77; 26, Created
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE EbiP8849 (Fragment).
GN Name=ebiG8849; ORFNames=ENSANGG00000006666;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=18045;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008986; BAA00365.1; -
FT NON_TER 1
FT NON_TER 1289
SQ SEQUENCE 1289 AA; 143051 MW; D97EC15A661BE3BD CRC64;

Query Match 86.5%; Score 32; DB 2; Length 1289;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
||||:||||
Db 362 GVAANSALF 370

RESULT 8
Q73XM1 PRELIMINARY; PRT; 158 AA.
AC Q73XM1; 27, Created
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
DE OrderedLocusNames=Map2288c;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;

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RN SEQUENCE FROM N.A.
 RP STRAIN=k10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017235; AAS04605.1; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 158 AA; 16266 MW; 2B63DC649F12A95B CRC64;

Query Match 83.8%; Score 31; DB 2; Length 158;
 Best Local Similarity 77.8%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
 |||||
 Db 127 GVAASSAF 135

RESULT 9
 AAS04605
 ID AAS04605 PRELIMINARY; PRT; 158 AA.
 AC AAS04605;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN MAP2288C.
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=k10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017235; AAS04605.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 158 AA; 16266 MW; 2B63DC649F12A95B CRC64;

Query Match 83.8%; Score 31; DB 2; Length 158;
 Best Local Similarity 77.8%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
 |||||
 Db 127 GVAASSAF 135

RESULT 10
 Q9CC58
 ID Q9CC58 PRELIMINARY; PRT; 163 AA.
 AC Q9CC58;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein ML1255.
 GN OrderedLocusNames=ML1255;
 OS Mycobacterium lepreae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
 RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Brown D., Chillingworth T., Connor R.,
 RA Mungall K.L., Basham D., Davis R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus."
 RL Nature 408:1007-1011(2001).
 DR EMBL; AL583921; CAC31636.1; -.
 DR PIR; A87066; A87066.
 DR Leproma; ML1255; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 163 AA; 16942 MW; F26ALA2C04E3FD2E CRC64;

Query Match 83.8%; Score 31; DB 2; Length 163;
 Best Local Similarity 77.8%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9
 |||||
 Db 132 GVAASSAF 140

RESULT 11
 OS3195
 ID OS3195 PRELIMINARY; PRT; 167 AA.
 AC OS3195; O7D735;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein MT2543.
 GN OrderedLocusNames=MT2543; RV2468c;
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/311159;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
 RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
 RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
 RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
 RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
 RA Rogers J., Rutter S., Seeger K., Skelton J., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RX MEDLINE=22206494; PubMed=12218036;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., M.D.,
 RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva H.M.,
 RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
 RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
 RA Fraser C.M.;
 RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL J. Bacteriol. 184:5479-5490(2002).
 DR EMBL; BX842579; CAAL6045.1; -.
 DR EMBL; AE007091; AAK46843.1; -.
 DR PIR; C70866; C70866.
 DR TIGR; MT2543; -.
 DR Tuberculist; RV2468c; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 167 AA; 17288 MW; F600B6FCA54E4BB4 CRC64;

Query Match 83.8%; Score 31; DB 2; Length 167;
 Best Local Similarity 77.8%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVAAXSSLF 9

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Db      136 GVAASSAF 144
|||||
Query Match      83.8%; Score 31; DB 2; Length 169;
Best Local Similarity 77.8%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GVAAXSSLF 9
      |||||
Db      138 GVAASSAF 146
      |||||

RESULT 14
Q9LE76 PRELIMINARY; PRT; 255 AA.
AC Q9LE76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OC NCBI_TaxID=39947;
CX [1]
SEQUENCE FROM N.A.
RN Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikano M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saij S., Sakai, K., Shibata M.,
RA Shinokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP001081; BAA90367.1; -.
DR EMBL; AF001073; BAA9586.1; -.
DR Gramene; Q9LE76; -.
KW Hypothetical protein.
SQ SEQUENCE 255 AA; 26887 MW; 0CA5C39B9987549 CRC64;

Query Match      83.8%; Score 31; DB 2; Length 255;
Best Local Similarity 77.8%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GVAAXSSLF 9
      |||||
Db      82 GVAPTSSLF 90
      |||||

RESULT 15
Q6KB71 PRELIMINARY; PRT; 191 AA.
AC Q6KB71;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-kafirin precursor.
GN Name=bkaf;
DE Sorghum bicolor (sorghum) (sorghum vulgare).
OS Sorghum bicolor (sorghum) (sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Sorghum.
OC NCBI_TaxID=4558;
CX [1]
SEQUENCE FROM N.A.
RN Chamba B., Halford N.G., Wilkinson M., Shewry P.R.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AJ717660; CAG30668.1; -.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001954; Glia glutenin.
 DR InterPro; IPR000480; Glutelin.
 DR Pfam; PF00234; Tryp.alpha.amyl; 1.
 DR PRINTS; PR00208; GLIADGLUTEN.
 DR PRINTS; PR00211; GLUTELIN.
 DR SMART; SM00499; AAI; 1.
 KW Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 191 beta-kafirin.
 SQ SEQUENCE 191 AA; 20605 MW; A99F952C9E2C311F CRC64;

Query Match 81.1%; Score 30; DB 2; Length 191;
 Best Local Similarity 87.5%; Pred.No. 1.le+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GVAAXSSL 8
 |||||
 Db 123 GVAAXSSL 130

Search completed: October 26, 2004, 16:04:59
 Job time : 43.6324 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:15 ; Search time 42.75 seconds
(without alignments)
75.522 Million cell updates/sec

Title: US-10-032-950-4

Perfect score: 37

Sequence: 1 AVNAXSLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	94.6	9	3	AAy67854 S. aureus
2	35	94.6	9	5	AAm50902 AgrD-auto
3	35	94.6	9	5	ABp53543 Cyclic pe
4	32	86.5	9	3	AAy67860 Staphyloc
5	32	86.5	9	3	AAy67859 Staphyloc
6	32	86.5	9	5	ABb07160 Peptide-m
7	32	86.5	9	5	AAm50907 Protected
8	32	86.5	9	5	AAm51004 AgrD2 lac
9	32	86.5	9	5	AAm51003
10	32	86.5	9	5	AAm51002
11	31	83.8	9	3	AAy67851 S. aureus
12	31	83.8	9	3	AAy67861 Staphyloc
13	31	83.8	9	5	ABb07161 Peptide-m
14	31	83.8	9	5	AAm51005 AgrD2 lac
15	31	83.8	9	5	AAm50908 Protected
16	31	83.8	9	5	AAm50899 AgrD-auto
17	31	83.8	9	5	ABp53540 Cyclic pe
18	31	83.8	61	7	ADf04608 Bacterial
19	31	83.8	549	4	AAb31559 Fimaricin
20	31	83.8	926	7	ADK62934 Disease t
21	30	81.1	9	2	AAW38323 Transcrip
22	30	81.1	9	5	ABb07159 Peptide-m
23	30	81.1	9	5	AAm51001 AgrD2 thi
24	30	81.1	9	5	AAm51001 S. aureus
25	30	81.1	9	6	ADf09190 S. aureus

26	30	81.1	9	8	ADJ98875	Peptide t
27	30	81.1	47	6	ABb84634	S. aureus
28	30	81.1	47	7	ADf09193	S. aureus
29	30	81.1	100	7	ADe09086	Novel pro
30	30	81.1	100	7	ADe09265	Novel pro
31	30	81.1	154	4	AAb60112	Human tra
32	30	81.1	171	3	AAg04535	Arabidops
33	30	81.1	171	3	AAg49535	Arabidops
34	30	81.1	183	3	AAg49534	Arabidops
35	30	81.1	183	3	AAg04534	Arabidops
36	30	81.1	229	7	ADe08057	Novel pro
37	30	81.1	316	4	ABg23871	Novel hum
38	30	81.1	335	3	AAg49533	Arabidops
39	30	81.1	335	3	AAg04533	Arabidops
40	30	81.1	335	5	ABb91365	Herbicida
41	30	81.1	335	8	ADN74713	Thale cre
42	30	81.1	339	7	ADe08283	Novel pro
43	30	81.1	345	6	ABg75820	Transport
44	30	81.1	572	5	AAU76036	Human sug
45	30	81.1	572	7	ADD37440	Human tra

ALIGNMENTS

RESULT 1

AAy67854

ID AAY67854 standard; peptide; 9 AA.

XX

AC AAY67854;

DT 25-APR-2000 (first entry)

XX

DE S. aureus peptide #4 used for bacterial interference.

XX

KW Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;

KX virulence factor; treatment.

XX

OS Staphylococcus aureus.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal residue forms bond with C-terminal

FT residue to form a cyclic peptide"

FT Misc-difference 5

FT /label= Unknown

XX

PN WO9967286-A2.

XX

PD 29-DEC-1999.

 XX | XX || PF | 24-JUN-1999; | 99WO-US014562. |
XX	XX	
PR	24-JUN-1998;	98US-00103438.
XX	XX	
PA	(UYRQ) UNIV ROCKEFELLER.	
PA	(UYNV) UNIV NEW YORK STATE.	
XX	XX	
PI	Muir TW, Mayville P, Novick RP, Ji G, Beavis R;	
XX	XX	
DR	WPI; 2000-147202/13.	
XX	XX	
PT	New cyclic peptides for treating infections with Staphylococcus aureus.	
XX	XX	
PS	Claim 9; Page 26; 37pp; English.	
XX	XX	
CC	This sequence represents a cyclic peptide derived from the Staphylococcus	
CC	aureus AgrD peptide. The invention relates to AgrD derived peptides, a	
CC	composition containing a peptide and a carrier, and a method for the	
CC	production of the cyclic peptides. The peptide inhibits the agr response,	
CC	which is normally associated with the release of virulence factors of	
CC	Staphylococcus aureus. An AgrD peptide is produced by S. aureus that	
CC	activates the agr response in strains of a single group, but interferes	

CC with this response in strains of different groups. The peptides and
 CC composition containing them can be used to treat infections by *S. aureus*
 XX
 SQ Sequence 9 AA;

Query Match 94.6%; Score 35; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
 DB 1 AVNAXSSLF 9

RESULT 2

AAM50902

ID AAM50902 standard; peptide; 9 AA.

XX

AC AAM50902;

DT 08-MAY-2002 (first entry)

DE AgrD-autoinducing cyclic peptide, inhibitor of agr response.

XX Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;

KW antibacterial; infection; therapy; cyclic.

XX

XX Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 5

FT /note= "note linked to residue 9 to form cyclic peptide"

FT Misc-difference 5

FT /note= "any amino acid"

FT Misc-difference 9

FT /note= "note linked to residue 5 to form cyclic peptide"

XX

XX US6337385-B1.

XX

XX 08-JAN-2002.

XX

XX 24-JUN-1999; 99US-00339511.

XX

XX 24-JUN-1998; 98US-0090402P.

XX (UYRQ) UNIV ROCKEFELLER.

XX (UYNY) UNIV NEW YORK STATE.

XX

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX WPI; 2002-170774/22.

XX

XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial

XX interference and for treating Staphylococcus aureus infection in a

XX subject.

XX

XX Disclosure; Col 17-18; 18pp; English.

XX

XX The present sequence is that of a novel synthetic cyclic peptide of the

XX invention that is capable of inhibiting the agr response of

XX Staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is

XX a secreted agr-encoded peptide and where the agr locus controls the

XX synthesis of virulence factor and other extracellular proteins

XX responsible for pathogenicity in *S. aureus*. Preferred peptides may haveXX the sequence NH₂-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z

XX residue and COOH other than a thioester bond, where X is an amino acid,

XX an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a

XX synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The

XX cyclic bond is especially a lactam or lactone bond. The thiolactone

XX structure within native AgrD peptides is required for activation of the

XX agr response. Elimination of the thiol ester component of the cyclic ring

XX structure can destroy agr response activating activity while preserving

XX and enhancing inhibitory activity. A claimed method of preparing a cyclic

CC peptide involves: assembling a linear peptide chain on to a solid phase
 CC resin support; deprotecting the resulting protected assembled peptide;
 CC treating the deprotected peptide with neutral buffer for a time
 CC sufficient to form the cyclic peptide and cleave the peptide from the
 CC support; and recovering the cyclic peptide. The peptide is useful for
 CC bacterial interference, especially for the treatment of *S. aureus*
 CC infection

XX Sequence 9 AA;

Query Match 94.6%; Score 35; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9

DB 1 AVNAXSSLF 9

RESULT 3

ABP53543

ID ABP53543 standard; peptide; 9 AA.

XX

AC ABP53543;

XX

DT 13-DEC-2002 (first entry)

XX

DE Cyclic peptide SEQ ID NO:4.

XX

KW Cyclic peptide; Staphylococcus aureus; infection; antibacterial;

XX agr response inhibitor.

XX

XX Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 5

FT /note= "any amino acid"

XX

XX US2002077453-A1.

XX

XX 20-JUN-2002.

XX

XX 27-DEC-2001; 2001US-00032950.

XX

XX 24-JUN-1998; 98US-0090402P.

XX

XX 24-JUN-1999; 99US-00339511.

XX

XX (MUIR/) MUIR T W.

XX (MAYV/) MAYVILLE P.

XX (NOVI/) NOVICK R P.

XX (BEAV/) BEAVIS R.

XX (JIGG/) JI G.

XX

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX WPI; 2002-681366/73.

XX

XX New cyclic peptides, useful for treating Staphylococcus aureus

XX infections.

XX

XX Claim 9; Page 10; 18pp; English.

XX

XX ABP53540 to ABP53547 represent cyclic peptides (I) from the present

XX invention. The present invention also describes a method for treating

XX Staphylococcus aureus infection comprising the administration of a

XX composition comprising (I). (I) has antibacterial activity, and can be

XX used as an agr gene response inhibitor. The peptides are useful for

XX treating *S. aureus* infections

XX

XX Sequence 9 AA;

Query Match

94.6%; Score 35; DB 5; Length 9;

Best Local Similarity

100.0%; Pred. No. 1.7e+06;

XX DR WPI; 2002-075235/10.
 XX PT Use of autoinducer-2 agonists or antagonists for regulating activity of
 PT autoinducer-2 receptor, regulating bacterial growth and pathogenesis,
 PT also antibiotic compositions.
 XX PS Disclosure; Page 33; 134pp; English.
 XX CC The invention relates to the use of autoinducer-2 (AI-2) agonists or
 CC antagonists for regulating activity of autoinducer-2 receptor, regulating
 CC bacterial growth and pathogenesis. Synergistic antibiotic compositions
 CC comprising inhibitors of the quorum-sensing pathway of a microorganism
 CC are also provided. Methods using such AI-2 analogues are useful for
 CC treating pathogen-associated disease states. The compounds and antibiotic
 CC compositions can be used to inhibit bacterial cell growth and/or biofilm
 CC formation on a medical device, particularly for promoting growth of skin
 CC graft replacements used in the treatment of burns and ulcers. They may
 CC also be used to aid wound repair, and to inhibit bacterial cell growth
 CC and biofilm formation in or on products or devices used for personal
 CC hygiene. The present sequence represents an inhibitor of peptide-mediated
 CC quorum sensing
 XX SQ Sequence 9 AA;

Query Match 86.5%; Score 32; DB 5; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSSLF 9
 ||| ||||
 Db 2 VNAXSSSLF 9

RESULT 7
 AAM50907
 ID AAM50907 standard; peptide; 9 AA.
 AC AAM50907;
 DT 08-MAY-2002 (first entry)
 DE Protected peptide used in cyclic peptide production.
 KW Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
 KW antibacterial; infection; therapy; cyclic.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "Z-Gly"
 FT Misc-difference 5
 FT Modified-site 5 /note= "note linked to residue 9 to form cyclic peptide"
 FT Modified-site 6 /note= "Ser(tBu)"
 FT Modified-site 6 /note= "Ser(Bzl)"
 FT Modified-site 7 /note= "Ser(Bzl)"
 FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"
 FT US6337385-B1.
 PN 08-JAN-2002.
 XX 24-JUN-1999; 99US-00339511.
 XX 24-JUN-1998; 98US-0090402P.
 XX (UVRQ) UNIV ROCKEFELLER.
 XX (UVNY) UNIV NEW YORK STATE.

XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
 XX WPI; 2002-170774/22.
 DR Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 PT interference and for treating Staphylococcus aureus infection in a
 PT subject.
 XX PS Disclosure; Col 14; 18pp; English.
 XX CC The present sequence is that of a protected peptide used in an example of
 CC the preparation of novel synthetic cyclic peptides of the invention (see
 CC AAM50899-906). The peptide corresponds to the Staphylococcus aureus
 CC AgrDII sequence with a Cys5 to Ser mutation (lactone). It was synthesised
 CC on a Wang-resin using an Fmoc N-alpha protection strategy. Following
 CC chain assembly, the peptide was cleaved from the support and the Ser-5
 CC residue deprotected by treatment with a trifluoroacetic
 CC acid:anisole:water mixture (90:5:5) for 4 hr. The partially protected
 CC peptide-alpha carboxylates were then dissolved in DMF and treated with
 CC PyBOP and a catalytic amount of dimethylaminopyridine. Cyclization was
 CC complete after 2 hr. The remaining protecting groups were then removed by
 CC treatment with HF and the peptide purified by HPLC. The cyclic peptide is
 CC capable of inhibiting the agr response of Staphylococcus aureus. The
 CC thiolactone structure within native AgrD peptides is required for
 CC activation of this response. Replacement of the thiol ester component of
 CC the cyclic ring structure with a lactone (as in the present case) or a
 CC lactam can destroy agr response activating activity while preserving and
 CC enhancing inhibitory activity. The cyclic peptides are useful for
 CC bacterial interference, especially for the treatment of S. aureus
 CC infection
 XX SQ Sequence 9 AA;

Query Match 86.5%; Score 32; DB 5; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSSLF 9
 ||| ||||
 Db 2 VNAXSSSLF 9

RESULT 8
 AAM51004
 ID AAM51004 standard; peptide; 9 AA.
 AC AAM51004;
 DT 07-AUG-2003 (revised)
 DT 08-MAY-2002 (first entry)
 DE AgrD2 lactone cyclic peptide.
 XX AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
 KW therapy; lactone; cyclic.
 OS Staphylococcus aureus.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"
 FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"
 FT US6337385-B1.
 PN 08-JAN-2002.
 XX 24-JUN-1999; 99US-00339511.
 XX 24-JUN-1998; 98US-0090402P.


```

XX PA (UYRQ ) UNIV ROCKEFELLER.
XX PA (UYNV ) UNIV NEW YORK STATE.
XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX XX WPI; 2002-170774/22.
DR DR
XX XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
XX PT interference and for treating Staphylococcus aureus infection in a
XX PT subject.
XX XX Example 1; Col 9; 18pp; English.
XX XX
XX XX The present sequence is that of a novel synthetic AgrD2 lactone cyclic
XX CC peptide in which residue 5 of the peptide is linked to residue 9 via a
XX CC lactone bond. The peptide is derived from an AgrD2 peptide of
XX CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
XX CC where the agr locus controls the synthesis of virulence factor and other
XX CC extracellular proteins responsible for pathogenicity in S. aureus. The
XX CC biological activity of the synthetic peptide was assayed using cultured
XX CC S. aureus strains containing a beta-lactamase reporter gene fused to the
XX CC agrP3 promoter. This allowed activation or inhibition of the agr response
XX CC to be monitored spectrophotometrically. The lactone AgrD2 peptide
XX CC inhibited the agr response of group I S. aureus strains without
XX CC activating the agr response in group I, II or III strains. The invention
XX CC provides claimed cyclic peptides (see AAM50899-906 and AAM50999) and
XX CC methods for preparing them, especially peptides where the cyclic bond is
XX CC a lactam or lactone bond. The cyclic peptides are useful for bacterial
XX CC interference, especially for the treatment of S. aureus infection.
XX CC (Updated on 07-AUG-2003 to correct OS field.)
XX XX
XX SQ Sequence 9 AA;
XX
Query Match 86.5%; Score 32; DB 5; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSSLF 9
Db 2 VNASSSLF 9

RESULT 9
AAM51003
ID AAM51003 standard; peptide; 9 AA.
XX AC AAM51003;
XX DT 08-MAY-2002 (first entry)
XX DE AgrD2 linear free acid peptide.
XX XX AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
XX KW therapy.
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX XX US6337385-B1.
XX XX 08-JAN-2002.
XX PF 24-JUN-1999; 99US-00339511.
XX XX 24-JUN-1998; 98US-0090402P.
XX XX (UYRQ ) UNIV ROCKEFELLER.
XX XX (UYNV ) UNIV NEW YORK STATE.
XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX XX WPI; 2002-170774/22.

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XX XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
XX PT interference and for treating Staphylococcus aureus infection in a
XX PT subject.
XX XX Example 1; Col 9; 18pp; English.
XX XX
XX XX The present sequence is that of a novel synthetic AgrD2 linear free acid
XX CC peptide. The peptide is derived from the cyclic AgrD2 peptide of
XX CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
XX CC where the agr locus controls the synthesis of virulence factor and other
XX CC extracellular proteins responsible for pathogenicity in S. aureus. The
XX CC biological activity of the synthetic peptide was assayed using cultured
XX CC S. aureus strains containing a beta-lactamase reporter gene fused to the
XX CC agrP3 promoter. This allowed activation or inhibition of the agr response
XX CC to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone
XX CC cyclic peptide (see AAM51001), the present peptide was unable to either
XX CC activate or inhibit the agr response, even when added to cultured cells
XX CC at 1M concentrations. The invention provides claimed cyclic peptides (see
XX CC AAM50899-906 and AAM50999) and methods for preparing them. The cyclic
XX CC peptides are useful for bacterial interference, especially for the
XX CC treatment of S. aureus infection
XX XX
XX SQ Sequence 9 AA;
XX
Query Match 86.5%; Score 32; DB 5; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSSLF 9
Db 2 VNASSSLF 9

RESULT 10
AAM51002
ID AAM51002 standard; peptide; 9 AA.
XX AC AAM51002;
XX DT 08-MAY-2002 (first entry)
XX DE AgrD2 linear thioester peptide.
XX XX AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
XX KW therapy.
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX XX Key Location/Qualifiers
XX FT Modified-site 9 /note="C-terminal thioester"
XX FT US6337385-B1.
XX XX 08-JAN-2002.
XX XX 24-JUN-1999; 99US-00339511.
XX XX 24-JUN-1998; 98US-0090402P.
XX XX (UYRQ ) UNIV ROCKEFELLER.
XX XX (UYNV ) UNIV NEW YORK STATE.
XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX XX WPI; 2002-170774/22.
XX XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
XX PT interference and for treating Staphylococcus aureus infection in a
XX PT subject.
XX XX

```

PS Example 1; Col 9; 18pp; English.

XX The present sequence is that of a novel synthetic AgrD2 linear thioester
CC peptide. The peptide is derived from the cyclic AgrD2 peptide of
CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
CC where the agr locus controls the synthesis of virulence factor and other
CC extracellular proteins responsible for pathogenicity in *S. aureus*. The
CC biological activity of the synthetic peptide was assayed using cultured
CC *S. aureus* strains containing a beta-lactamase reporter gene fused to the
CC agrP3 promoter. This allowed activation or inhibition of the agr response
CC to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone
CC cyclic peptide (see AM51001), the present peptide was unable to either
CC activate or inhibit the agr response, even when added to cultured cells
CC at μM concentrations. The invention provides claimed cyclic peptides (see
CC AM50899-906 and AM50999) and methods for preparing them. The cyclic
CC peptides are useful for bacterial interference, especially for the
CC treatment of *S. aureus* infection

XX Sequence 9 AA;

Query Match 86.5%; Score 32; DB 5; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSSLF 9
||| |||||
DB 2 VNAXSSSLF 9

RESULT 11
AAAY67851
ID AAAY67851 standard; peptide; 9 AA.

XX AC AAAY67851;

XX DT 25-APR-2000 (first entry)

XX DE *S. aureus* peptide #1 used for bacterial interference.

XX KW Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;
XX virulence factor; treatment.

XX OS Staphylococcus aureus.

XX FH Key Location/Qualifiers

XX FT Misc-difference 5

XX FT /label= Unknown

XX PN WO9967286-A2.

XX XX 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-US014562.

XX PR 24-JUN-1998; 98US-00103438.

XX PA (UYRQ) UNIV ROCKEFELLER.

XX PA (UYNY) UNIV NEW YORK STATE.

XX PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX DR WPI; 2000-147202/13.

XX FT New cyclic peptides for treating infections with Staphylococcus aureus.

XX PS Claim 9; Page 26; 37pp; English.

XX CC This sequence represents a cyclic peptide derived from the Staphylococcus
CC aureus AgrD peptide. The invention relates to AgrD derived peptides, a
CC composition containing a peptide and a carrier, and a method for the
CC production of the cyclic peptides. The peptide inhibits the agr response,
CC which is normally associated with the release of virulence factors of
CC Staphylococcus aureus. An AgrD peptide is produced by *S. aureus* that

CC activates the agr response in strains of a single group, but interferes
CC with this response in strains of different groups. The peptides and
CC composition containing them can be used to treat infections by *S. aureus*
XX Sequence 9 AA;

Query Match 83.8%; Score 31; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VNAXSSSLF 9
|||||||
DB 2 VNAXSSSLF 9

RESULT 12
AAAY67861
ID AAAY67861 standard; peptide; 9 AA.

XX AC AAAY67861;

XX DT 25-APR-2000 (first entry)

XX DE Staphylococcus aureus AgrDII derived peptide sequence.

XX KW Staphylococcus aureus infection; AgrD; agr response; treatment;
XX virulence factor.

XX OS Staphylococcus aureus.

XX FH Key Location/Qualifiers

XX FT Misc-difference 5

XX FT /label= Unknown

XX PN WO9967286-A2.

XX XX 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-US014562.

XX PR 24-JUN-1998; 98US-00103438.

XX PA (UYRQ) UNIV ROCKEFELLER.

XX PA (UYNY) UNIV NEW YORK STATE.

XX PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX DR WPI; 2000-147202/13.

XX FT New cyclic peptides for treating infections with Staphylococcus aureus.

XX PS Example; Page 22; 37pp; English.

XX CC This sequence represents the Staphylococcus aureus AgrDII derived
CC peptide. The invention relates to AgrD derived cyclic peptides, a
CC composition containing a peptide and a carrier, and a method for the
CC production of the cyclic peptides. The peptide inhibits the agr response,
CC which is normally associated with the release of virulence factors of
CC Staphylococcus aureus. An AgrD peptide is produced by *S. aureus* that
CC activates the agr response in strains of a single group, but interferes
CC with this response in strains of different groups. The peptides and
CC composition containing them can be used to treat infections by *S. aureus*

XX Sequence 9 AA;

Query Match 83.8%; Score 31; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VNAXSSSLF 9
|||||||
DB 2 VNAXSSSLF 9

[illegible]

XX AC AM50908;
XX DE 08-MAY-2002 (first entry)
XX DT Protected peptide used in cyclic peptide production.
XX DE Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
XX KW antibacterial; infection; therapy; cyclic.
XX KW Synthetic.
XX OS
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Z-Gly"
XX FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"
XX FT Modified-site 5 /label= Dpr(Boc)
XX FT Modified-site 6 /note= "Ser(Bzl)"
XX FT Modified-site 7 /note= "Ser(Bzl)"
XX FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"
XX FT
XX FN US637385-B1.
XX PN
XX XX
XX PD 08-JAN-2002.
XX PF 24-JUN-1999; 99US-00339511.
XX PR 24-JUN-1998; 98US-0090402P.
XX PA (UYRQ) UNIV ROCKEFELLER.
XX PA (UYNV) UNIV NEW YORK STATE.
XX FI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX DR WPI; 2002-170774/22.
XX DR
XX PT Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
XX PT interference and for treating Staphylococcus aureus infection in a
XX PT subject.
XX FS Disclosure; Col 14; 18pp; English.
XX CC
XX CC The present sequence is that of a protected peptide used in an example of
XX CC the preparation of novel synthetic cyclic peptides of the invention (see
XX CC AM50899-906). The peptide corresponds to the Staphylococcus aureus
XX CC AgrDII sequence with a Cys to diaminopropionic acid (Dpr) mutation
XX CC (lactam). It was synthesised on a Wang-resin using an Fmoc N-alpha
XX CC protection strategy. Following chain assembly, the peptide was cleaved
XX CC from the support and the Dpr-5 residue deprotected by treatment with a
XX CC trifluoroacetic acid:anisole:water mixture (90:5:5) for 4 hr. The
XX CC partially protected peptide-alpha carboxylates were then dissolved in DMF
XX CC and treated with PyBOP. Cyclization was complete after 2 hr. The
XX CC remaining protecting groups were removed by treatment with HF and the
XX CC peptide purified by HPLC. The cyclic peptide is capable of inhibiting the
XX CC agr response of Staphylococcus aureus. The thiolactone structure within
XX CC native AgrD peptides is required for activation of this response.
XX CC Replacement of the thiol ester component of the cyclic ring structure
XX CC with a lactam (as in the present case) or a lactone can destroy agr
XX CC response activating activity while preserving and enhancing inhibitory
XX CC activity. The cyclic peptides are useful for bacterial interference,
XX CC especially for the treatment of S. aureus infection
XX CC
XX SQ Sequence 9 AA;

Query Match 83.8%; Score 31; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VNAXSSLF 9
Db 2 VNAXSSLF 9
Search completed: October 26, 2004, 15:59:42
Job time : 43.75 secs .

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2004, 15:54:00 ; Search time 31.5 Seconds
(without alignments)
92.502 Million cell updates/sec

Title: US-10-032-950-4

Perfect score: 37

Sequence: 1 AVNAXSLF 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	94.6	9	13	US-10-032-950-4
2	34	91.9	633	14	US-10-369-493-6225
3	31	83.8	9	13	US-10-032-950-1
4	30	81.1	9	14	US-10-201-444-3
5	30	81.1	47	14	US-10-201-444-6
6	30	81.1	130	15	US-10-424-599-206201
7	30	81.1	140	16	US-10-767-701-44650
8	30	81.1	265	16	US-10-767-701-46660
9	30	81.1	298	15	US-10-425-114-64168
10	30	81.1	303	16	US-10-437-963-174739
11	30	81.1	343	15	US-10-424-599-168046
12	30	81.1	538	16	US-10-437-963-151317
13	30	81.1	572	9	US-09-919-781-2

14	81.1	572	14	US-10-154-419-13	Sequence 13, Appl
15	81.1	832	15	US-10-424-599-196029	Sequence 196029,
16	78.4	132	15	US-10-424-599-229061	Sequence 229061,
17	78.4	426	15	US-10-289-762-760	Sequence 760, App
18	78.4	605	14	US-10-100-303A-110	Sequence 110, App
19	78.4	740	15	US-10-282-122A-49115	Sequence 49115, A
20	78.4	1054	14	US-10-369-493-1849	Sequence 1849, Ap
21	78.4	1054	15	US-10-462-698A-2	Sequence 2, Appli
22	78.4	1054	15	US-10-462-698A-4	Sequence 4, Appli
23	78.4	1054	15	US-10-462-698A-6	Sequence 6, Appli
24	78.4	1054	15	US-10-450-941-8	Sequence 8, Appli
25	78.4	1054	15	US-10-450-941-12	Sequence 12, Appli
26	78.4	1054	15	US-10-450-941-14	Sequence 14, Appli
27	78.4	1054	15	US-10-041-018-168	Sequence 168, App
28	78.4	1054	15	US-10-041-018-311	Sequence 311, App
29	75.7	9	13	US-10-032-950-5	Sequence 5, Appli
30	75.7	9	13	US-10-032-950-6	Sequence 6, Appli
31	75.7	25	16	US-10-416-249-492	Sequence 492, App
32	75.7	55	16	US-10-786-778-8	Sequence 8, Appli
33	75.7	78	13	US-10-078-929-136	Sequence 136, App
34	75.7	162	16	US-10-437-963-176513	Sequence 176513,
35	75.7	248	14	US-10-369-493-14264	Sequence 14264, A
36	75.7	248	14	US-10-369-493-14770	Sequence 14770, A
37	75.7	257	14	US-10-369-493-11482	Sequence 11482, A
38	75.7	322	15	US-10-485-114-47039	Sequence 47039, A
39	75.7	340	15	US-10-282-122A-72850	Sequence 72850, A
40	75.7	441	14	US-10-369-493-2265	Sequence 2265, Ap
41	75.7	526	14	US-10-369-493-3924	Sequence 3924, Ap
42	75.7	561	13	US-10-078-929-138	Sequence 138, App
43	75.7	1200	15	US-10-282-122A-54407	Sequence 54407, A
44	73.0	9	13	US-10-032-950-2	Sequence 2, Appli
45	73.0	61	14	US-10-029-386-27613	Sequence 27613, A

ALIGNMENTS

RESULT 1
US-10-032-950-4
; Sequence 4, Application US/10032950
; Publication NO. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032, 950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-4

Query Match 94.6%; Score 35; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVNAXSLF 9

Db
1 AVNAXSLF 9

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RESULT 2
US-10-369-493-6225
/ Sequence 6225, Application US/10369493
/ Publication No. US20030233675A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MITO
/ CHROMOSOMAL DNA IN PLANTS WITH IMPRO
/ FILE REFERENCE: 38-10(52052) B
/ CURRENT APPLICATION NUMBER: US/10/369
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,0
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO 6225
/ LENGTH: 633
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-10-369-493-6225

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Query Match          91.9%; Score 34; DB 14; Length 633;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7: Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 AVNAXSSLF 9
|:| | | |
Dp 327 AINAFSSLF 3

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RESULT 3
US-10-032-950-1
; Sequence 1, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Mullr, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this posit
US-10-032-950-1

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Query Match 83.8%; Score 31; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VNAXSSLF 9

Db 2 VNAXSSLF 9

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RESULT 4
US-10-201-444-3
; Sequence 3: Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FIELD REFERENCE: 6375377
; CURRENT APPLICATION NUMBER: US/10/201,444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-201-444-3

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Query Match      81.1%; Score 30; DB 14; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 2 VNAXSLF 9
||| |||
pb 2 VNACSSLF 9

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RESULT 5
US-10-201-444-6
, Sequence 6, Application US/10201444
, Publication NO. US20030078378A1
, GENERAL INFORMATION:
, APPLICANT: New York University Medical Center
, TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
, FILE REFERENCE: 63753/7
, CURRENT APPLICATION NUMBER: US/10/201,444
, CURRENT FILING DATE: 2002-07-23
, PRIOR APPLICATION NUMBER: US/08/861,476
, PRIOR FILING DATE: 1997-05-22
, NUMBER OF SEQ ID NOS: 8
, SOFTWARE: PatentIn version 3.0
, SEQ ID NO 6
, LENGTH: 47
, TYPE: PRT
, ORGANISM: Staphylococcus aureus
, US-10-201-444-6

```

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Query Match      81.1%; Score 30; DB 14; Length 47;
Best Local Similarity 87.5%; Pred. No. 22;
Matches 7: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 VNAXSSLF 9
Db 25 VNACSSLF 32

RESULT 6
US-10-424-599-206201
; Sequence 206201, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yungwei
; TITLE OF INVENTION: Soy Nucleic Acid Mo
; TITLE OF INVENTION: plants and Uses Th

FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206201
LENGTH: 130
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(130)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_28226C.1.pep
US-10-424-599-206201

Query Match 81.1%; Score 30; DB 15; Length 130;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
|:|:| |

Db 87 AINAISLF 95

RESULT 7

US-10-767-701-44650
Sequence 44650, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 44650
LENGTH: 140
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C740_1.pep
US-10-767-701-44650

Query Match 81.1%; Score 30; DB 16; Length 140;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
|:|:| |

Db 127 AINAISLF 135

RESULT 8

US-10-767-701-46660
Sequence 46660, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 46660
LENGTH: 265
TYPE: PRT

ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C104_77.pep
US-10-767-701-46660

Query Match 81.1%; Score 30; DB 16; Length 265;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
|:|:| |

Db 17 AVNPSSLF 25

RESULT 9

US-10-425-114-64168
Sequence 64168, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64168
LENGTH: 298
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3593-001-E12_FLI.pep
US-10-425-114-64168

Query Match 81.1%; Score 30; DB 15; Length 298;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
|:|:| |

Db 285 AINAISLF 293

RESULT 10

US-10-437-963-174739
Sequence 174739, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 174739
LENGTH: 303
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_72652C.1.pep

US-10-437-963-174739

Query Match 81.1%; Score 30; DB 16; Length 303;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
|:|:|:|:|
DB 290 AINAISL 298

RESULT 11

US-10-424-599-168046
; Sequence 168046, Application US/10424599
; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 168046

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(343)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_122761C.1.pap

US-10-424-599-168046

Query Match 81.1%; Score 30; DB 15; Length 343;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
|:|:|:|:|
DB 330 AINAISL 338

RESULT 12

US-10-437-963-151317
; Sequence 151317, Application US/10437963
; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barzak, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 151317

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_51471C.1.pap

US-10-437-963-151317

Query Match 81.1%; Score 30; DB 16; Length 538;
Best Local Similarity 77.8%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
|:|:|:|:|
DB 328 AFNASSSLF 336

RESULT 13

US-09-919-781-2

; Sequence 2, Application US/09919781

; Patent No. US20020123094A1

; GENERAL INFORMATION:

; APPLICANT: Curtis, Roy A.J.

; TITLE OF INVENTION: 57250, A NOVEL HUMAN SUGAR TRANSPORTER

; FILE REFERENCE: YMI-181

; CURRENT APPLICATION NUMBER: US/09/919,781

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: USSN 60/221,769

; PRIOR FILING DATE: 2000-07-31

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 572

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-919-781-2

Query Match 81.1%; Score 30; DB 9; Length 572;
Best Local Similarity 77.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
|:|:|:|:|
DB 453 AVSALSSLF 461

RESULT 14

US-10-154-419-13

; Sequence 13, Application US/10154419

; Publication No. US20030143675A1

; GENERAL INFORMATION:

; APPLICANT: Curtis, Roy A.J.

; APPLICANT: Glucksman, Maria Alexandra

; APPLICANT: Meyers, Rachel E.

; TITLE OF INVENTION: NOVEL 38594, 57312, 53659, 57250, 63760, 49938, 32146,

; TITLE OF INVENTION: 57259, 67118, 67067, 62092, 8099, 46455, 54414, 53763,

; TITLE OF INVENTION: 67076, 67102, 44181, 67084FL, 67084ALT, FHS58295FL, 57255,

; TITLE OF INVENTION: AND 57255alt MOLECULES AND USES THEREFOR

; FILE REFERENCE: YMI-249

; CURRENT APPLICATION NUMBER: US/10/154,419

; CURRENT FILING DATE: 2002-05-22

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: FastSeq Version 4.0

; SEQ ID NO 13

; LENGTH: 572

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-154-419-13

Query Match 81.1%; Score 30; DB 14; Length 572;
Best Local Similarity 77.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
|:|:|:|:|
DB 453 AVSALSSLF 461


```
RESULT 15
US-10-424-599-196029
; Sequence 196029, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(59223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 196029
; LENGTH: 832
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(832)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_1903C.1.pep
US-10-424-599-196029

Query Match      81.1%; Score 30; DB 15; Length 832;
Best Local Similarity 77.8%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AVNAXSLF 9
      |||||
Db      387 AVNPFSSLF 395
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Search completed: October 26, 2004, 16:10:12
Job time : 32.5 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2004, 15:46:55 ; Search time 8.73529 Seconds
(without alignments)
99.132 Million cell updates/sec

Title: US-10-032-950-4

Perfect score: 37

Sequence: 1 AVNAXSSLF 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	91.9	633	2 T27215	hypothetical prote
2	32	86.5	2055	2 T31617	hypothetical prote
3	31	83.8	413	2 AH2933	N-carbamoyl-beta-a
4	31	83.8	441	2 G98348	N-carbamoyl-beta-a
5	31	83.8	926	2 S48463	SEC24 protein-ye
6	30	81.1	47	2 C89995	AgrD protein [impo
7	30	81.1	265	2 SI3098	chlorophyll a/b-bi
8	30	81.1	315	2 A96597	hypothetical prote
9	30	81.1	1016	2 T30943	aminopeptidase (EC
10	30	81.1	1016	2 T30942	aminopeptidase (EC
11	29	78.4	271	2 P90350	lysosomal membrane
12	29	78.4	382	2 A28057	120K lysosomal mem
13	29	78.4	405	2 A60534	cholesterol oxidase
14	29	78.4	407	2 A32000	DNA topoisomerase
15	29	78.4	546	2 A32260	DNA gyrase, chain
16	29	78.4	599	2 D70104	DNA gyrase subunit
17	29	78.4	602	2 C72043	alpha-mannosidase
18	29	78.4	602	2 H86579	hydroxymethylgluta
19	29	78.4	1049	2 T30525	probable short-cha
20	29	78.4	1054	2 A30239	dehydrogenase/redu
21	28	75.7	273	2 H98193	hypothetical prote
22	28	75.7	273	2 AB3093	hypothetical prote
23	28	75.7	292	2 AH2082	ferrichrome ABC tr
24	28	75.7	333	1 C69812	hypothetical prote
25	28	75.7	497	2 S57145	hypothetical prote
26	28	75.7	1200	2 AB1343	DNA-directed DNA p
27	27	73.0	76	2 T26894	hypothetical prote
28	27	73.0	195	2 T46291	hypothetical prote
29	27	73.0	251	2 AB1222	cobalamin adenosyl

30 27 73.0 251 2 AH1575 cobalamin adenosyl
31 27 73.0 260 2 B97225 probable endonucle
32 27 73.0 301 2 E92333 conserved hypothet
33 27 73.0 368 2 AB2215 hypothetical prote
34 27 73.0 379 2 S76029 hypothetical prote
35 27 73.0 492 2 F70339 glycerol kinase -
36 27 73.0 541 2 D94779 probable 3-ketoacy
37 27 73.0 570 2 T33320 hypothetical prote
38 27 73.0 573 2 T27578 hypothetical prote
39 27 73.0 726 2 T15810 hypothetical prote
40 27 73.0 756 2 T38683 hypothetical prote
41 27 73.0 760 2 E83610 conserved hypothet
42 27 73.0 842 2 A87557 non-motile and pha
43 27 73.0 842 2 S27533 histidine protein
44 27 73.0 957 2 A47531 glutamyl aminopept
45 27 73.0 993 2 A38437 probable homeotic

ALIGNMENTS

RESULT 1

T27215 hypothetical protein Y57G11C.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T27215

R;McMurray, A.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z20330

A;Accession: T27215

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-633 <WIL>

A;Cross-references: UNIPROT:O19227; EMBL:Z99281; PIDN:CAB16503.1; GSPDB:GN00022; CESP:Y

A;Experimental source: clone Y57G11C

C;Genetics:

A;Gene: CESP:Y57G11C.1

A;Map position: 4

A;Introns: 70/1; 329/3

C;Superfamily: multidrug resistance protein; ATP-binding cassette homology

Query Match 91.9%; Score 34; DB 2; Length 633;

Best Local Similarity 77.8%; Pred. No. 3.8;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9

Db 327 AINAFSSLP 335

RESULT 2

T31617 hypothetical protein Y50E8A.m - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T31617

R;Steward, C.

submitted to the EMBL Data Library, September 1999

A;Reference number: Z21047

A;Accession: T31617

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2055 <WIL>

A;Cross-references: EMBL:AL117200; NID:el549770; PIDN:CAB55056.1; CESP:Y50E8A.m

A;Experimental source: clone Y50E8A

C;Genetics:

A;Gene: CESP:Y50E8A.m

A;Introns: 273/3; 447/1; 526/1; 735/1; 1247/1; 1418/1; 1494/1; 1753/3

Query Match 86.5%; Score 32; DB 2; Length 2055;

Best Local Similarity 77.8%; Pred. No. 44;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVNAXSLF 9
 1751 AUNAFSLF 1759

RESULT 3
 AH2933
 N-carbamoyl-beta-alanine amidohydrolase [imported] - Agrobacterium tumefaciens (strain C)
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AH2933
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AH2933
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-413 <KUR>
 A:Cross-references: UNIPROT:Q8UB66; GB:AE008689; PIDN:AA443886.1; PID:g17741433; GSPDB:C
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: amaB
 A:Map position: linear chromosome
 C:Superfamily: N-carbamyl-L-amino acid amidohydrolase

Query Match 83.8%; Score 31; DB 2; Length 413;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVNAXSLF 9
 246 AVNALGSLF 254

RESULT 4
 G98348
 n-carbamoyl-beta-alanine amidohydrolase PA0444 [imported] - Agrobacterium tumefaciens (B)
 C:Species: Agrobacterium tumefaciens
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: G98348
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: G98348
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-441 <KUR>
 A:Cross-references: UNIPROT:Q8UB66; GB:AE007870; PIDN:AAK90313.1; PID:g15160344; GSPDB:C
 C:Genetics:
 A:Gene: AGR_L3478
 A:Map position: linear chromosome
 C:Superfamily: N-carbamyl-L-amino acid amidohydrolase

Query Match 83.8%; Score 31; DB 2; Length 441;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVNAXSLF 9
 274 AVNALGSLF 282

RESULT 5
 S48463
 SEC24 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YIL109C
 C:Species: Saccharomyces cerevisiae
 C>Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
 C:Accession: S48463
 R:Bowman, S.; Churcher, C.
 submitted to the EMBL Data Library, September 1994
 A:Reference number: S48455
 A:Accession: S48463
 A:Molecule type: DNA
 A:Residues: 1-926 <BOW>
 A:Cross-references: UNIPROT:P40482; GB:Z47047; EMBL:Z38125; NID:g603997; PID:g763237; GSPDB:C
 C:Genetics:
 A:Gene: SGD:SEC24; SEC24; MIPS:YIL109C
 A:Cross-references: MIPS:YIL109C; SGD:S0001371
 A:Map position: 9L
 C:Function:
 A:Description: involved in endoplasmic reticulum to Golgi transport; required for vesicle

Query Match 83.8%; Score 31; DB 2; Length 926;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSLF 9
 787 INATSSLF 794

RESULT 6
 C89995
 AgRD protein [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: C89995
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yurawa, H.; Kobayashi, I.; Cui, L.; Oguc, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: C89995
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-47 <KUR>
 A:Cross-references: UNIPROT:O33586; GB:BA000018; PID:g13701831; PIDN:BA43124.1; GSPDB:C
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: agrD

Query Match 81.1%; Score 30; DB 2; Length 47;
 Best Local Similarity 87.5%; Pred. No. 2;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSLF 9
 25 VNACSLF 32

RESULT 7
 S13098
 chlorophyll a/b-binding protein precursor - maize
 C:Species: Zea mays (maize)
 C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S13098
 R:Viret, J.F.; Schantz, M.L.; Schantz, R.
 Nucleic Acids Res. 18, 7179, 1990
 A:Title: Nucleotide sequence of a maize cDNA coding for a light-harvesting chlorophyll a
 A:Reference number: S13098; MUID:91088340; PMID:2263499
 A:Accession: S13098
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-265 <VIR>
 A:Cross-references: UNIPROT:P27497; EMBL:X55892; NID:g22354; PIDN:CAA39376.1; PID:g22355
 C:Superfamily: chlorophyll a/b-binding protein

C;Keywords: chloroplast; thylakoid; transmembrane protein

Query Match 81.1%; Score 30; DB 2; Length 265;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
||| |||

DB 17 AVNVPSSLF 25

RESULT 8

A96597

Hypothetical protein TSA14.12 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: A96597

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A96597

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-315 <SFO>

A;Cross-references: UNIPROT:Q92VU6; GB:AE005173; NID:g4204267; PIDN:AAD10648.1; GSPDB:GN

C;Genetics:

A;Gene: TSA14.12

A;Map position: 1

Query Match 81.1%; Score 30; DB 2; Length 315;

Best Local Similarity 66.7%; Pred. No. 17;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
||| |||

DB 302 AINAISLF 310

RESULT 9

T30943

aminopeptidase (EC 3.4.11.-) - Indian meal moth

C;Species: Plodia interpunctella (Indian meal moth)

C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C;Accession: T30943

R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.

submitted to the EMBL Data Library, November 1997

A;Description: Molecular comparison of aminopeptidase cDNAs and gene structure between b

A;Reference number: Z20942

A;Accession: T30943

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1016 <ZHU>

A;Cross-references: UNIPROT:O17485; EMBL:AF034484; NID:g2645994; PID:g2645995; PIDN:AA3

C;Superfamily: membrane alanyl aminopeptidase

C;Keywords: aminopeptidase

Query Match 81.1%; Score 30; DB 2; Length 1016;

Best Local Similarity 66.7%; Pred. No. 61;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
||| |||

DB 152 AVNATSALF 160

RESULT 10

T30942

aminopeptidase (EC 3.4.11.-) - Indian meal moth

C;Species: Plodia interpunctella (Indian meal moth)

C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C;Accession: T30942

R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.

submitted to the EMBL Data Library, November 1997

A;Description: Molecular comparison of aminopeptidase cDNAs and gene structure between t

A;Reference number: Z20942

A;Accession: T30942

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1016 <ZHU>

A;Cross-references: UNIPROT:O17484; EMBL:AF034483; NID:g2645992; PID:g2645993; PIDN:AA3

C;Superfamily: membrane alanyl aminopeptidase

C;Keywords: aminopeptidase

Query Match 81.1%; Score 30; DB 2; Length 1016;

Best Local Similarity 66.7%; Pred. No. 61;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
||| |||

DB 152 AVNATSALF 160

RESULT 11

F90350

Hypothetical protein SSO1873 [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Date: 24-May-2000 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: F90350

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: F90350

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-271 <KUR>

A;Cross-references: UNIPROT:Q97X81; GB:AE006641; NID:gl3815127; PIDN:AAK42061.1; GSPDB:

C;Genetics:

A;Gene: SSO1873

Query Match 78.4%; Score 29; DB 2; Length 271;

Best Local Similarity 66.7%; Pred. No. 25;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9
||| |||

DB 249 SVNSDSSLF 257

RESULT 12

A28067

lysosomal membrane glycoprotein LAMP-1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C;Accession: A28067

R;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T.

J. Biol. Chem. 263, 8754-8758, 1988

A;Title: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprot

A;Reference number: A28067; MUID:88243732; PMID:3379044

A;Accession: A28067

A;Molecule type: mRNA

A;Residues: 1-382 <CHE>

A;Cross-references: UNIPROT:P11438; GB:J03881; NID:cl98706; PIDN:AAA39411.1; PID:g29369

A;Note: the authors translated the codon ATT for residue 1 as Leu and CCG for residue 2

C;Superfamily: lysosome-associated membrane protein

C;Keywords: glycoprotein; membrane protein

Query Match 78.4%; Score 29; DB 2; Length 382;
 Best Local Similarity 75.0%; Pred. No. 36;
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Qy 2 VNAXSSSLF 9
 :|||
 Db 257 MNASSSLF 264

RESULT 13

A60534
 P2B/LAMP-1 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C:Accession: A60534
 R:Heffernan, M.; Yousefi, S.; Dennis, J.W.
 Cancer Res. 49, 6077-6084, 1989
 A>Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastasi
 A:Reference number: A60534; MUID:90002989; PMID:2676155
 A:Accession: A60534
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-405 <REF>
 A:Cross-references: UNIPROT:P11438
 C:Superfamily: lysosome-associated membrane protein

Query Match 78.4%; Score 29; DB 2; Length 405;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Qy 2 VNAXSSSLF 9
 :|||
 Db 280 MNASSSLF 287

RESULT 14

A30200
 120K lysosomal membrane glycoprotein precursor - rat
 N:Alternate names: sialoglycoprotein
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: A30200; S03331
 R:Howe, C.L.; Granger, B.L.; Hull, M.; Green, S.A.; Gabel, C.A.; Helenius, A.; Mellman,
 Proc. Natl. Acad. Sci. U.S.A. 85, 7577-7581, 1988
 A>Title: Derived protein sequence, oligosaccharides, and membrane insertion of the 120-k
 glycoproteins.
 A:Reference number: A30200; MUID:89017240; PMID:3174652
 A:Accession: A30200
 A:Molecule type: mRNA
 A:Residues: 1-407 <HOW>
 A:Cross-references: UNIPROT:P14562; EMBL:J03672
 A>Note: the authors translated the codon GGG for residue 15 as Val
 R:Himeno, M.; Noguchi, Y.; Sakaki, H.; Tanaka, Y.; Furuno, K.; Kono, A.; Sakaki, Y.; Kad
 FEBS Lett. 244, 351-356, 1989
 A>Title: Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in
 A:Reference number: S03331; MUID:89153580; PMID:2920835
 A:Accession: S03331
 A:Molecule type: mRNA
 A:Residues: 22-407 <HIM>
 A:Cross-references: EMBL:X14765; NID:956577; PIDN:CAA32873.1; PID:956578
 A>Note: part of this sequence, including the amino end of the mature protein, was confir
 C:Superfamily: lysosome-associated membrane protein
 C:Keywords: glycoprotein; membrane protein
 F:22-407/Product: lysosomal membrane glycoprotein, 107K #status experimental <MAT>

Query Match 78.4%; Score 29; DB 2; Length 407;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Qy 2 VNAXSSSLF 9
 :|||
 Db 282 MNATSSSLF 289

RESULT 15

A32260
 cholesterol oxidase (BC 1.1.3.6) precursor [validated] - Streptomyces sp.
 C:Species: Streptomyces sp.
 C>Date: 20-Oct-1989 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
 C:Accession: A32260; S15810; PC2002
 R:Shizaki, T.; Hirayama, N.; Shinkawa, H.; Nimi, O.; Murooka, Y.
 J. Bacteriol. 171, 596-601, 1989
 A>Title: Nucleotide sequence of the gene for cholesterol oxidase from a Streptomyces sp.
 A:Reference number: A32260; MUID:89123081; PMID:2914858
 A:Accession: A32260
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 'V', 2-546 <ISH>
 A:Cross-references: UNIPROT:P12676; GB:M31939; GB:J03356; NID:9153210; PIDN:AAA26719.1;
 A>Note: the authors translated the initiation codon GTG for residue 1 as Val
 R:Horii, M.; Ishizaki, T.; Faik, S.Y.; Manome, T.; Murooka, Y.
 J. Bacteriol. 172, 3644-3653, 1990

A>Title: An operon containing the genes for cholesterol oxidase and a cytochrome P-450-1
 A:Reference number: S15809; MUID:90299781; PMID:2361941
 A:Accession: S15810
 A:Molecule type: DNA
 A:Residues: 1-30 <HOR>

A:Cross-references: EMBL:M31939; GB:J03356; NID:9153210
 R:Furcell, J.P.; Greenplate, J.T.; Jennings, M.G.; Rysse, J.S.; Pershing, J.C.; Sims, S
 Biochem. Biophys. Res. Commun. 196, 1406-1413, 1993
 A>Title: Cholesterol oxidase: a potent insecticidal protein active against boll weevil 1
 A:Reference number: PC2002; MUID:94071904; PMID:8250897

A:Accession: PC2002
 A:Molecule type: protein
 A:Residues: 'XXXTF', 48-54, 'XX', 57, 'X', 59-60 <PUR>
 C:Genetics:
 A:Gene: choA

C:Keywords: oxidoreductase
 F:1-42/Domain: signal sequence #status predicted <SIG>
 F:43-546/Product: cholesterol oxidase #status experimental <MAT>

Query Match 78.4%; Score 29; DB 2; Length 546;
 Best Local Similarity 66.7%; Pred. No. 54;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVNAXSSSLF 9
 :|||
 Db 446 AVNAAKALF 454

Search completed: October 26, 2004, 16:06:08
 Job time : 9.73529 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:50 ; Search time 40.6324 Seconds
(without alignments)
127.445 Million cell updates/sec

Title: US-10-032-950-4

Perfect score: 37

Sequence: 1 AVNAXSSLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	91.9	633	018227	018227 caenorhabdi
2	32	86.5	549	06T3C4	06T3C4 streptomyce
3	32	86.5	549	AAR16516	AAR16516 streptomy
4	32	86.5	807	09U275	09U275 caenorhabdi
5	31	83.8	413	08UBB6	08UBB6 agrobacteri
6	31	83.8	441	07CR15	07CR15 agrobacteri
7	31	83.8	549	09EW96	09EW96 streptomyce
8	31	83.8	891	075B16	075B16 ashbya goss
9	31	83.8	891	AAS51681	AAS51681 ashbya go
10	31	83.8	926	SC24_YEAST	P40482 saccharomyc
11	30	81.1	47	033586	033586 staphylococ
12	30	81.1	47	07A2N4	07A2N4 staphylococ
13	30	81.1	47	07A417	07A417 staphylococ
14	30	81.1	47	CAE92745	CAE92745 staphyloc
15	30	81.1	47	CAE92748	CAE92748 staphyloc
16	30	81.1	47	CAE92751	CAE92751 staphyloc
17	30	81.1	47	CAE92754	CAE92754 staphyloc
18	30	81.1	47	CAE92757	CAE92757 staphyloc
19	30	81.1	111	0710P9	0710P9 oryza sativ
20	30	81.1	111	CAD23149	CAD23149 oryza sat
21	30	81.1	150	092214	092214 coprinus ci
22	30	81.1	219	06YV56	06YV56 oryza sativ
23	30	81.1	219	BAC84585	BAC84585 oryza sat
24	30	81.1	240	09LKK3	09LKK3 oryza sativ
25	30	81.1	265	1 CB29_MAIZE	1 CB29_MAIZE zeam mays
26	30	81.1	267	1 PROB_STRTR	1 PROB_STRTR streptococ
27	30	81.1	315	09ZVU6	09ZVU6 arabidopsis
28	30	81.1	335	06YV55	06YV55 oryza sativ
29	30	81.1	335	08L972	08L972 arabidopsis
30	30	81.1	335	094BS2	094BS2 arabidopsis
31	30	81.1	335	2 BAC84586	2 BAC84586 oryza sat

32	30	81.1	356	2	Q9SRW2	Q9erm2 arabidopsis
33	30	81.1	358	2	Q9C780	Q9c780 arabidopsis
34	30	81.1	359	2	Q9AT39	Q9at39 glycine max
35	30	81.1	371	2	Q8GX26	Q8gx26 arabidopsis
36	30	81.1	1016	2	017484	017484 plodia inte
37	30	81.1	1016	2	017485	017485 plodia inte
38	29	78.4	143	2	Q8EFG6	Q8efg6 shewanella
39	29	78.4	189	2	Q922T9	Q922t9 mus musculu
40	29	78.4	261	2	Q9KJF3	Q9kjp3 myxococcus
41	29	78.4	271	2	Q97X81	Q97x81 sulfolobus
42	29	78.4	406	1	LMPI_MOUSE	LMPI38 mus musculu
43	29	78.4	406	2	Q8VH34	Q8vh34 mus musculu
44	29	78.4	407	1	LMPI_RAT	PI4562 rattus norv
45	29	78.4	407	2	Q9DCI3	Q9dc13 mus musculu

ALIGNMENTS

RESULT 1

ID	018227	PRELIMINARY;	PRT;	633 AA.
AC	018227			
DT	01-JAN-1998	(Tremblrel. 05, Created)		
DT	01-JAN-1998	(Tremblrel. 05, Last sequence update)		
DT	01-OCT-2003	(Tremblrel. 25, Last annotation update)		
DE	Hypothetical protein Y57G11C.1.			
GN	Name=Y57G11C.1;			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Pelodirinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	McMurray A.A.;			
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBSJ databases.			
RT	- !- SIMILARITY: Belongs to the ABC transporter family.			
RL	EMBL; 299281; CAB16503.1; -			
RT	PIR; T27215; T27215.			
DR	HSP; P08716; IMT0.			
DR	WormPep; Y57G11C.1; CE14926.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.			
DR	GO; GO:0000166; F:nucleotide binding; IEA.			
DR	GO; GO:0006810; P:transport; IEA.			
DR	InterPro; IPR003593; AAA_ATPase.			
DR	InterPro; IPR011527; ABC_membrane_1.			
DR	InterPro; IPR001140; ABC_TM_transp.			
DR	InterPro; IPR003439; ABC_transporter.			
DR	Pfam; PF00664; ABC_membrane; 1.			
DR	Pfam; PF00005; ABC_tran; 1.			
DR	SMART; SM00382; AAA_1.			
DR	PROSITE; PS50329; ABC_TM1F; 1.			
DR	PROSITE; PS00211; ABC_TRANSPORTER_1; 1.			
DR	PROSITE; PS50893; ABC_TRANSPORTER_2; 1.			
KW	ATP-binding; Hypothetical protein.			
SK	SEQUENCE 633 AA; 71699 MW; 8807414AA9884058 CRC64;			

Query Match 91.9%; Score 34; DB 2; Length 633;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVNAXSSLF 9

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Db 327 AINAFSLF 335
|:|:| |
RESULT 2
Q6T2C4 PRELIMINARY; PRT; 549 AA.
AC Q6T2C4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Rind.
GN Name=rmd;
OS Streptomyces diastaticus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=108;
RA Seco E.M., Perez-Zuniga F.J., Malpartida F.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY442225; AAR16516.1; -.
DR InterPro; IPR000172; GMC_oxred.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
DR PROSITE; PS00623; GMC_OXRED_1; -.
SQ SEQUENCE 549 AA; 59306 MW; 7719F5D7D47D0683 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 549;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVNAXSLF 9
|:|:| |
Db 449 AVNAKSLF 457

RESULT 3
AAR16516 PRELIMINARY; PRT; 549 AA.
AC AAR16516;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Rind.
GN RIND.
OS Streptomyces diastaticus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=108;
RA Seco E.M., Perez-Zuniga F.J., Malpartida F.;
RL "Two tetraenes macrolides (rimocidin and CE-108) are derived from the
RT same biosynthetic pathway in Streptomyces diastaticus var. 108:
RT Partial characterization of the biosynthetic gene cluster and
RT deduction of their biosynthetic steps.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY442225; AAR16516.1; -.
SQ SEQUENCE 549 AA; 59306 MW; 7719F5D7D47D0683 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 549;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVNAXSLF 9
|:|:| |
Db 449 AVNAKSLF 457

RESULT 4

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Q9U275 PRELIMINARY; PRT; 807 AA.
AC Q9U275;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein Y50E8A.16.
GN Name=Y50E8A.16;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Steward C.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AL117200; CAB60586.1; -.
DR HSSP; Q03518; 1J37.
DR WormPep; Y508A.16; CE24404.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR011527; AAA_ATPase.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABC_tm_transpt.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR SMART; SMO0382; AAA; 1.
DR PROSITE; PS0929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS0693; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Hypothetical protein.
SQ SEQUENCE 807 AA; 91162 MW; B9ABC598966DF1EF CRC64;

Query Match 86.5%; Score 32; DB 2; Length 807;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVNAXSLF 9
|:|:| |
Db 503 ALNAPSLF 511

RESULT 5
Q8UBE6 PRELIMINARY; PRT; 413 AA.
AC Q8UBE6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE N-carbamoyl-beta-alanine amidohydrolase.
GN Name=amaB; OrderedLocustNames=Atu3070;
OC Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193;

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RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen I.T., Eisele J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
DR EMBL; AE009237; AAL43886.1; -.
DR PIR; AH2933; AH2933.
DR PIR; G98348; G98348.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR010158; Hydantase.
DR InterPro; IPR002933; Peptidase M20.
DR Pfam; PF01546; Peptidase_M20; 1.
DR TIGRFAMs; TIGR01879; Hydantase; 1.
KW Complete proteome; Hydantase.
SQ SEQUENCE 413 AA; 44639 MW; 4678CB631023B659 CRC64;

Query Match 83.8%; Score 31; DB 2; Length 413;
Best Local Similarity 77.8%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVNAXSSLF 9
Db 246 AVNALGSLF 254

RESULT 6
ID Q7CR15 PRELIMINARY; PRT; 441 AA.
AC Q7CR15;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AGR_L_3478p.
GN OrderedLocuNames=AGR_L_3478;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cereon;
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houniel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL; AE008376; AAK90313.1; -.
DR InterPro; IPR010158; Hydantase.
DR InterPro; IPR002933; Peptidase_M20.
DR Pfam; PF01546; Peptidase_M20; 1.
DR TIGRFAMs; TIGR01879; Hydantase; 1.
SQ SEQUENCE 441 AA; 47628 MW; 7AD50CF34F86410F CRC64;

Query Match 83.8%; Score 31; DB 2; Length 441;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVNAXSSLF 9

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Db 274 AVNALGSLF 282

RESULT 7
ID Q9EW96 PRELIMINARY; PRT; 549 AA.
AC Q9EW96;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PimE protein.
GN Name=pimE;
OS Streptomyces natalensis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=68242;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20547809; PubMed=11094342;
RA Aparicio J.F., Fouces R., Mendes M.V., Olivera N., Martin J.F.;
RT "A complex multienzyme system encoded by five polyketide synthase
RT genes is involved in the biosynthesis of the 26-membered polyene
RT macrolide pimarinin in Streptomyces natalensis.";
RL Chem. Biol. 7:895-905(2000).
DR EMBL; AJ278573; CAC20926.1; -.
DR HSP; P12676; IMXT.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000172; GMC_oxred.
DR InterPro; IPR006311; Tat.
DR TIGRFAMs; TIGR01409; TAT signal_seq; 1.
DR PROSITE; PS00623; GMC_OXRED_1; 1.
SQ SEQUENCE 549 AA; 59475 MW; 96759DE780AC5A82 CRC64;

Query Match 83.8%; Score 31; DB 2; Length 549;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVNAXSSLF 9
Db 449 AVNARSULF 457

RESULT 8
ID Q75B16 PRELIMINARY; PRT; 891 AA.
AC Q75B16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ADL239Cp.
GN Name=ADL239C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetaceae; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RX PubMed=15001715;
RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
RA Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome.";
RL Science 304:304-307(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Voegelé S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
RA Philippsen P.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

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FT HELIX 153
FT HELIX 165
FT TURN 179
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FT HELIX 849
FT TURN 859
FT STRAND 870
FT HELIX 890
FT TURN 901
FT TURN 903
FT TURN 908
FT HELIX 913
SQ SEQUENCE 926 AA; 103635 MW; 35E2BDD24CC75899 CRC64;

Query Match 83.8%; Score 31; DB 1; Length 926;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSLF 9
Db 787 INATSSLF 794

RESULT 11

OC33586 PRELIMINARY; PRT; 47 AA.
AC OC33586;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE AgrD.
GN Name=agrD;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=1280;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=SA502A;
RX MEDLINE=97342847; PubMed=9197262;
RA Ji G., Beavis R., Novick R.P.;
RT "Bacterial interference caused by autoinducing peptide variants."
RL Science 276:2027-2030(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Gt31a-cp5, Gt31b-cp5, Gt36a-cp8, Gt36b-cp8, and Gt111-cp8;
RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF001782; AAB63265.1; -
DR EMBL; AJ617715; CAE92745.1; -
DR EMBL; AJ617716; CAE92748.1; -
DR EMBL; AJ617717; CAE92751.1; -
DR EMBL; AJ617718; CAE92754.1; -
DR EMBL; AJ617719; CAE92757.1; -
DR FIR; C89995; C89995.
DR InterPro; IPR009229; AgrD.
DR Pfam; PF05931; AgrD; 1.
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF548FA7 CRC64;

Query Match 81.1%; Score 30; DB 2; Length 47;

Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSLF 9
Db 25 VNACSSLF 32

RESULT 12
Q7A2N4 PRELIMINARY; PRT; 47 AA.
ID Q7A2N4
AC Q7A2N4
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE AgrD protein.
GN Name=agrD; OrderedLocusNames=SAV2037;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yanashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003364; BABS8199.1; -.
DR InterPro; IPR009229; AgrD.
DR Pfam; PF05931; AgrD; 1.
KW Complete proteome.
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 81.1%; Score 30; DB 2; Length 47;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSLF 9
Db 25 VNACSSLF 32

RESULT 13
Q7A4I7 PRELIMINARY; PRT; 47 AA.
ID Q7A4I7
AC Q7A4I7
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE AgrD protein.
GN Name=agrD; OrderedLocusNames=SA1842.1; ORFNames=SAS066;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yanashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).

DR EMBL; AP003135; BAB43124.1; -.
DR InterPro; IPR009229; AgrD.
DR Pfam; PF05931; AgrD; 1.
KW Complete proteome.
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 81.1%; Score 30; DB 2; Length 47;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSLF 9
Db 25 VNACSSLF 32

RESULT 14
CAE92745 PRELIMINARY; PRT; 47 AA.
ID CAE92745
AC CAE92745;
DT 01-APR-2004 (TRENBLrel. 27, Created)
DT 01-APR-2004 (TRENBLrel. 27, Last sequence update)
DT 01-APR-2004 (TRENBLrel. 27, Last annotation update)
DE AgrD protein.
GN AGRD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=gt31b-cp5;
RA Goerke C., Dabach S., Kuemmel M., Wolz C.;
RT "Evolutionary Models for the Development of the Polymorphic Loci agr
and cap in Staphylococcus aureus.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ617715; CAE92745.1; -.
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 81.1%; Score 30; DB 2; Length 47;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSLF 9
Db 25 VNACSSLF 32

RESULT 15
CAE92748 PRELIMINARY; PRT; 47 AA.
ID CAE92748
AC CAE92748;
DT 01-APR-2004 (TRENBLrel. 27, Created)
DT 01-APR-2004 (TRENBLrel. 27, Last sequence update)
DT 01-APR-2004 (TRENBLrel. 27, Last annotation update)
DE AgrD protein.
GN AGRD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=gt31b-cp5;
RA Goerke C., Dabach S., Kuemmel M., Wolz C.;
RT "Evolutionary Models for the Development of the Polymorphic Loci agr
and cap in Staphylococcus aureus.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ617716; CAE92748.1; -.
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 81.1%; Score 30; DB 2; Length 47;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSSLF 9
Db 25 VNACSSLF 32

Db ||| |||
 25 VNACSLF 32

Search completed: October 26, 2004, 16:05:01
Job time : 42.6324 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:15 ; Search time 42.75 Seconds
(without alignments)
75.522 Million cell updates/sec

Title: US-10-032-950-5

Perfect score: 39

Sequence: 1 GVNAASLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	94.9	9	3	AAY67855 S. aureus
2	37	94.9	9	5	AM50903 AgrD-auto
3	37	94.9	9	5	ABP53544 Cyclic pe
4	35	89.7	9	3	AAY67860 Staphyloc
5	35	89.7	9	3	AAY67859 Staphyloc
6	35	89.7	9	5	ABB07160 Peptide-m
7	35	89.7	9	5	AM50907 Protected
8	35	89.7	9	5	AM51004 AgrD2 lac
9	35	89.7	9	5	AM51003 AgrD2 lin
10	35	89.7	9	5	AM51002 AgrD2 lin
11	34	87.2	9	3	AAY67851 S. aureus
12	34	87.2	9	3	AAY67861 Staphyloc
13	34	87.2	9	5	ABB07161 Peptide-m
14	34	87.2	9	5	AM51005 AgrD2 lac
15	34	87.2	9	5	AM50908 Protected
16	34	87.2	9	5	AM50899 AgrD-auto
17	34	87.2	9	5	ABP53540 Cyclic pe
18	33	84.6	9	2	AAW38323 Transcrip
19	33	84.6	9	5	ABB07159 Peptide-m
20	33	84.6	9	5	AM51001 AgrD2 thi
21	33	84.6	9	6	ABB84631 S. aureus
22	33	84.6	9	7	ADP09190 S. aureus
23	33	84.6	9	8	ADJ98875 Peptide t
24	33	84.6	47	6	ABB84634 S. aureus
25	33	84.6	47	7	ADF09193 S. aureus

26	32	82.1	271	6	ABU44321 Protein e
27	32	82.1	490	7	ADH11546 Chimpanze
28	31	79.5	9	3	AAY67856 S. aureus
29	31	79.5	9	5	AM50904 AgrD-auto
30	31	79.5	9	5	ABP53545 Cyclic pe
31	31	79.5	1959	8	ADN36926 X. albili
32	30	76.9	9	3	AAY67852 S. aureus
33	30	76.9	9	5	AM50900 AgrD-auto
34	30	76.9	9	5	ABP53541 Cyclic pe
35	30	76.9	147	3	AB41086 Human ORF
36	30	76.9	147	5	ABP34694 Human ORF
37	30	76.9	339	7	ADC95277 E. faeciu
38	30	76.9	340	6	ABU25396 Protein e
39	30	76.9	347	6	ABU24755 Protein e
40	30	76.9	396	6	ABU35191 Protein e
41	30	76.9	415	7	ADC87185 Human GPC
42	30	76.9	432	7	ADC87445 Human GPC
43	30	76.9	464	7	ABO79302 Pseudomon
44	30	76.9	464	7	ABO78813 Pseudomon
45	30	76.9	552	4	ABG13082 Novel hum

ALIGNMENTS

RESULT 1

AAY67855

ID AAY67855 standard; peptide; 9 AA.

XX

AC AAY67855;

XX

DT 25-APR-2000 (first entry)

XX

DE S. aureus peptide #5 used for bacterial interference.

XX

KW Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;

KW virulence factor; treatment.

XX

OS Staphylococcus aureus.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal residue forms bond with C-terminal

FT residue to form a cyclic peptide"

FT Misc-difference 5

FT /label= Unknown

XX

PN WO9967286-A2.

XX

PD 29-DEC-1999.

XX

PF 24-JUN-1999; 99WO-US014562.

XX

PR 24-JUN-1998; 98US-00103438.

XX

PA (UYRQ) UNIV ROCKEFELLER.

PA (UYNY) UNIV NEW YORK STATE.

XX

PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX

DR WPI; 2000-147202/13.

 XX |

CC with this response in strains of different groups. The peptides and
 CC composition containing them can be used to treat infections by *S. aureus*
 XX
 SQ Sequence 9 AA;
 Query Match 94.9%; Score 37; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GVNAXASLF 9
 DB 1 GVNAXASLF 9
 RESULT 2
 AAM50903
 ID AAM50903 standard; peptide; 9 AA.
 XX
 AC AAM50903;
 DT 08-MAY-2002 (first entry)
 DE AgrD-autoinducing cyclic peptide, inhibitor of agr response.
 XX
 XX Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
 XX antibacterial; infection; therapy; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5
 FT /note= "note linked to residue 9 to form cyclic peptide"
 FT Misc-difference 5
 FT /note= "any amino acid"
 FT Misc-difference 9
 FT /note= "note linked to residue 5 to form cyclic peptide"
 FT
 XX US6337385-B1.
 XX
 XX 08-JAN-2002.
 XX
 XX 24-JUN-1999; 99US-00339511.
 XX
 XX 24-JUN-1998; 98US-0090402P.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 XX (UYNY) UNIV NEW YORK STATE.
 XX
 XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
 XX WPI; 2002-170774/22.
 XX
 XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 XX interference and for treating Staphylococcus aureus infection in a
 XX subject.
 XX
 XX Claim 7; Col 19; 18pp; English.
 XX
 XX The present sequence is that of a novel synthetic cyclic peptide of the
 XX invention that is capable of inhibiting the agr response of
 XX Staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is
 XX a secreted agr-encoded peptide and where the agr locus controls the
 XX synthesis of virulence factor and other extracellular proteins
 XX responsible for pathogenicity in *S. aureus*. Preferred peptides may have
 XX the sequence NH₂-X(n)-2-X(i)-COOH, with a cyclic bond between the Z
 XX residue and COOH other than a thioester bond, where X is an amino acid,
 XX an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a
 XX synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The
 XX cyclic bond is especially a lactam or lactone bond. The thiololactone
 XX structure within native AgrD peptides is required for activation of the
 XX agr response. Elimination of the thiol ester component of the cyclic ring
 XX structure can destroy agr response activating activity while preserving
 XX and enhancing inhibitory activity. A claimed method of preparing a cyclic

CC peptide involves: assembling a linear peptide chain on to a solid phase
 CC resin support; deprotecting the resulting protected assembled peptide;
 CC treating the deprotected peptide with neutral buffer for a time
 CC sufficient to form the cyclic peptide and cleave the peptide from the
 CC support; and recovering the cyclic peptide. The peptide is useful for
 CC bacterial interference, especially for the treatment of *S. aureus*
 CC infection
 XX
 SQ Sequence 9 AA;
 Query Match 94.9%; Score 37; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GVNAXASLF 9
 DB 1 GVNAXASLF 9
 RESULT 3
 ABP53544
 ID ABP53544 standard; peptide; 9 AA.
 XX
 AC ABP53544;
 DT 13-DEC-2002 (first entry)
 DE Cyclic peptide SEQ ID NO:5.
 XX
 XX Cyclic peptide; Staphylococcus aureus; infection; antibacterial;
 XX agr response inhibitor.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5
 FT /note= "any amino acid"
 FT
 XX US2002077453-A1.
 XX
 XX 20-JUN-2002.
 XX
 XX 27-DEC-2001; 2001US-00032950.
 XX
 XX 24-JUN-1998; 98US-0090402P.
 XX 24-JUN-1999; 99US-00339511.
 XX
 XX (MUIR/) MUIR T W.
 XX (MAVV/) MAYVILLE P.
 XX (NOVI/) NOVICK R P.
 XX (BEAV/) BEAVIS R.
 XX (JIGG/) JI G.
 XX
 XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
 XX WPI; 2002-681366/73.
 XX
 XX New cyclic peptides, useful for treating Staphylococcus aureus
 XX infections.
 XX
 XX Claim 9; Page 10; 18pp; English.
 XX
 XX ABP53540 to ABP53547 represent cyclic peptides (I) from the present
 XX invention. The present invention also describes a method for treating
 XX Staphylococcus aureus infection comprising the administration of a
 XX composition comprising (I). (I) has antibacterial activity and can be
 XX used as an agr gene response inhibitor. The peptides are useful for
 XX treating *S. aureus* infections
 XX
 SQ Sequence 9 AA;
 Query Match 94.9%; Score 37; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;


```

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXSLF 9
DB 1 GVNAXSLF 9

RESULT 4
AAV67860
ID AAV67860 standard; peptide; 9 AA.
AC AAV67860;
DT 25-APR-2000 (first entry)
DE Staphylococcus aureus AgrDII derived peptide sequence.
XX
KW Staphylococcus aureus infection; AgrD; agr response; treatment;
KW virulence factor.
OS Staphylococcus aureus.
XX
PN WO9967286-A2.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-US014562.
XX
PR 24-JUN-1998; 98US-00103438.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
PA (UYNY ) UNIV NEW YORK STATE.
XX
PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;
XX
DR WPI; 2000-147202/13.
XX
PT New cyclic peptides for treating infections with Staphylococcus aureus.
XX
PS Example; Page 22; 37pp; English.
XX
CC This sequence represents the Staphylococcus aureus AgrDII derived
CC peptide. The invention relates to AgrD derived cyclic peptides, a
CC composition containing a peptide and a carrier, and a method for the
CC production of the cyclic peptides. The peptide inhibits the agr response,
CC which is normally associated with the release of virulence factors of
CC Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
CC activates the agr response in strains of a single group, but interferes
CC with this response in strains of different groups. The peptides and
CC composition containing them can be used to treat infections by S. aureus
XX
SQ Sequence 9 AA;

Query Match 89.7%; Score 35; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. NO. 1.7e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSLF 9
DB 1 GVNAXSLF 9

RESULT 6
ABB07160
ID ABB07160 standard; peptide; 9 AA.
XX
AC ABB07160;
XX
DT 13-MAR-2002 (first entry)
XX
DE Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
XX
KW Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
KW vulnary; pheromone; agr system; accessory gene regulator; cyclic.
XX
OS Synthetic.
XX
PN WO200185664-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-US015221.
XX
PR 10-MAY-2000; 2000US-0203000P.
PR 07-DEC-2000; 2000US-0254398P.
XX
XX (UYPR-) UNIV PRINCETON.
PA (QUOR-) QUOREX PHARM INC.
PA (UYTE-) UNIV TECHNOLOGIES INT INC.
XX
PI Bassler BL, Dammel CS, Schauder S, Shokat K, Stein J, Surette MG;

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virulence factor.
XX
OS Staphylococcus aureus.
XX
PN WO9967286-A2.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-US014562.
XX
PR 24-JUN-1998; 98US-00103438.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
PA (UYNY ) UNIV NEW YORK STATE.
XX
PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;
XX
DR WPI; 2000-147202/13.
XX
PT New cyclic peptides for treating infections with Staphylococcus aureus.
XX
PS Example; Page 22; 37pp; English.
XX
CC This sequence represents the Staphylococcus aureus AgrDII derived
CC peptide. The invention relates to AgrD derived cyclic peptides, a
CC composition containing a peptide and a carrier, and a method for the
CC production of the cyclic peptides. The peptide inhibits the agr response,
CC which is normally associated with the release of virulence factors of
CC Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
CC activates the agr response in strains of a single group, but interferes
CC with this response in strains of different groups. The peptides and
CC composition containing them can be used to treat infections by S. aureus
XX
SQ Sequence 9 AA;

Query Match 89.7%; Score 35; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. NO. 1.7e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSLF 9
DB 1 GVNAXSLF 9

RESULT 6
ABB07160
ID ABB07160 standard; peptide; 9 AA.
XX
AC ABB07160;
XX
DT 13-MAR-2002 (first entry)
XX
DE Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
XX
KW Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
KW vulnary; pheromone; agr system; accessory gene regulator; cyclic.
XX
OS Synthetic.
XX
PN WO200185664-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-US015221.
XX
PR 10-MAY-2000; 2000US-0203000P.
PR 07-DEC-2000; 2000US-0254398P.
XX
XX (UYPR-) UNIV PRINCETON.
PA (QUOR-) QUOREX PHARM INC.
PA (UYTE-) UNIV TECHNOLOGIES INT INC.
XX
PI Bassler BL, Dammel CS, Schauder S, Shokat K, Stein J, Surette MG;

```

XX WPI; 2002-075235/10.
 XX
 XX Use of autoinducer-2 agonists or antagonists for regulating activity of
 FT autoinducer-2 receptor; regulating bacterial growth and pathogenesis;
 FT also antibiotic compositions.
 XX
 XX Disclosure; Page 33; 134pp; English.
 XX
 XX The invention relates to the use of autoinducer-2 (AI-2) agonists or
 CC antagonists for regulating activity of autoinducer-2 receptor, regulating
 CC bacterial growth and pathogenesis. Synergistic antibiotic compositions
 CC comprising inhibitors of the quorum-sensing pathway of a microorganism
 CC are also provided. Methods using such AI-2 analogues are useful for
 CC treating pathogen-associated disease states. The compounds and antibiotic
 CC compositions can be used to inhibit bacterial cell growth and/or biofilm
 CC formation on a medical device, particularly for promoting growth of skin
 CC graft replacements used in the treatment of burns and ulcers. They may
 CC also be used to aid wound repair, and to inhibit bacterial cell growth
 CC and biofilm formation in or on products or devices used for personal
 CC hygiene. The present sequence represents an inhibitor of peptide-mediated
 CC quorum sensing
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 89.7%; Score 35; DB 5; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GVNAXASLF 9
 |||||:
 DB 1 GVNASSSLF 9
 RESULT 7
 AAM50907
 ID AAM50907 standard; peptide; 9 AA.
 XX
 XX AAM50907;
 AC
 DT 08-MAY-2002 (first entry)
 XX
 XX Protected peptide used in cyclic peptide production.
 DE
 XX Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
 KW antibacterial; infection; therapy; cyclic.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "Z-Gly"
 FT
 FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"
 FT Modified-site 5 /note= "Ser(tBu)"
 FT Modified-site 6 /note= "Ser(Bzl)"
 FT Modified-site 7 /note= "Ser(Bzl)"
 FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"
 FT
 FT US6337385-B1.
 PN
 XX 08-JAN-2002.
 PD
 XX 24-JUN-1999; 98US-00339511.
 XX
 XX 24-JUN-1998; 98US-0090402P.
 PR
 XX (JYRQ) UNIV ROCKEFELLER.
 PA (JYNY) UNIV NEW YORK STATE.
 PA

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
 PI WPI; 2002-170774/22.
 XX
 XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 FT interference and for treating Staphylococcus aureus infection in a
 FT subject.
 XX
 XX Disclosure; Col 14; 18pp; English.
 PS
 XX The present sequence is that of a protected peptide used in an example of
 CC the preparation of novel synthetic cyclic peptides of the invention (see
 CC AAM50899-906). The peptide corresponds to the Staphylococcus aureus
 CC AgrDII sequence with a Cys5 to Ser mutation (lactone). It was synthesised
 CC on a Wang-resin using an Fmoc N-alpha protection strategy. Following
 CC chain assembly, the peptide was cleaved from the support and the Ser-5
 CC residue deprotected by treatment with a trifluoroacetic
 CC acid:anisole:water mixture (90:5:5) for 4 hr. The partially protected
 CC peptide-alpha carboxylates were then dissolved in DMF and treated with
 CC PyBOP and a catalytic amount of dimethylaminopyridine. Cyclization was
 CC complete after 2 hr. The remaining protecting groups were then removed by
 CC treatment with HF and the peptide purified by HPLC. The cyclic peptide is
 CC capable of inhibiting the agr response of Staphylococcus aureus. The
 CC thiolactone structure within native AgrD peptides is required for
 CC activation of this response. Replacement of the thiol ester component of
 CC the cyclic ring structure with a lactone (as in the present case) or a
 CC lactam can destroy agr response activating activity while preserving and
 CC enhancing inhibitory activity. The cyclic peptides are useful for
 CC bacterial interference, especially for the treatment of S. aureus
 CC infection
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 89.7%; Score 35; DB 5; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GVNAXASLF 9
 |||||:
 DB 1 GVNASSSLF 9
 RESULT 8
 AAM51004
 ID AAM51004 standard; peptide; 9 AA.
 XX
 XX AAM51004;
 AC
 XX 07-AUG-2003 (revised)
 DT 08-MAY-2002 (first entry)
 XX
 XX AgrD2 lactone cyclic peptide.
 DE
 XX AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
 KW therapy; lactone; cyclic.
 XX
 XX Staphylococcus aureus.
 OS
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"
 FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"
 FT
 FT US6337385-B1.
 PN
 XX 08-JAN-2002.
 PD
 XX 24-JUN-1999; 98US-00339511.
 XX
 XX 24-JUN-1998; 98US-0090402P.
 PR
 XX (JYRQ) UNIV ROCKEFELLER.
 PA (JYNY) UNIV NEW YORK STATE.
 PA

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XX (UYRQ ) UNIV ROCKEFELLER.
PA (UYNY ) UNIV NEW YORK STATE.
XX
PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX WPI; 2002-170774/22.
XX
XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
PT interference and for treating Staphylococcus aureus infection in a
PT subject.
XX
XX Example 1; Col 9; 18pp; English.
XX
XX The present sequence is that of a novel synthetic AgrD2 linear free acid
CC peptide in which residue 5 of the peptide is linked to residue 9 via a
CC lactone bond. The peptide is derived from an AgrD2 peptide of
CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
CC where the agr locus controls the synthesis of virulence factor and other
CC extracellular proteins responsible for pathogenicity in S. aureus. The
CC biological activity of the synthetic peptide was assayed using cultured
CC S. aureus strains containing a beta-lactamase reporter gene fused to the
CC agrP3 promoter. This allowed activation or inhibition of the agr response
CC to be monitored spectrophotometrically. The lactone AgrD2 peptide
CC inhibited the agr response in group I, II or III strains. The invention
CC provides claimed cyclic peptides (see AAM50899-906 and AAM50999) and
CC methods for preparing them, especially peptides where the cyclic bond is
CC a lactam or lactone bond. The cyclic peptides are useful for bacterial
CC interference, especially for the treatment of S. aureus infection.
CC (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 9 AA;

Query Match 89.7%; Score 35; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXASLF 9
   |||| :|||
Db 1 GVNASSSLF 9

RESULT 10
AAM51002
ID AAM51002 standard; peptide; 9 AA.
XX
AC AAM51002;
XX
DT 08-MAY-2002 (first entry)
XX
DE AgrD2 linear thioester peptide.
XX
KW AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
KW therapy.
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9 /note= "C-terminal thioester"
XX
PN US6337385-B1.
XX
XX 08-JAN-2002.
XX
XX 24-JUN-1999; 99US-00339511.
XX
XX 24-JUN-1998; 98US-0090402P.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
PA (UYNY ) UNIV NEW YORK STATE.
XX
XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX WPI; 2002-170774/22.
XX
XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
PT interference and for treating Staphylococcus aureus infection in a
PT subject.
XX

```

Example 1; Col 9; 18pp; English.

PS The present sequence is that of a novel synthetic AgrD2 linear thioester
 XX peptide. The peptide is derived from the cyclic AgrD2 peptide of
 CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
 CC where the agr locus controls the synthesis of virulence factor and other
 CC extracellular proteins responsible for pathogenicity in *S. aureus*. The
 CC biological activity of the synthetic peptide was assayed using cultured
 CC *S. aureus* strains containing a beta-lactamase reporter gene fused to the
 CC agrP3 promoter. This allowed activation or inhibition of the agr response
 CC to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone
 CC cyclic peptide (see AM51001), the present peptide was unable to either
 CC activate or inhibit the agr response, even when added to cultured cells
 CC at 10^6 concentrations. The invention provides claimed cyclic peptides (see
 CC AM50899-906 and AM50999) and methods for preparing them. The cyclic
 CC peptides are useful for bacterial interference, especially for the
 CC treatment of *S. aureus* infection

Sequence 9 AA;

Query Match 89.7%; Score 35; DB 5; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXASLIF 9
 DB 1 GVNAXSSSLF 9

RESULT 11

AAV67851
 ID AAV67851 standard; peptide; 9 AA;

XX AC AAV67851;

XX DT 25-APR-2000 (first entry)

XX DE *S. aureus* peptide #1 used for bacterial interference.

XX XX Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;
 KW virulence factor; treatment.

XX OS Staphylococcus aureus.

XX FH Key Location/Qualifiers

FT Misc-difference 5 /label= Unknown

XX WO9967286-A2.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-US014562.

XX PR 24-JUN-1998; 98US-00103438.

XX PA (UYRQ) UNIV ROCKEFELLER.

XX PA (UUNY) UNIV NEW YORK STATE.

XX PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX DR WPI; 2000-147202/13.

XX PT New cyclic peptides for treating infections with Staphylococcus aureus.

XX PS Claim 9; Page 26; 37pp; English.

XX This sequence represents a cyclic peptide derived from the Staphylococcus
 CC aureus AgrD peptide. The invention relates to AgrD derived peptides, a
 CC composition containing a peptide and a carrier, and a method for the
 CC production of the cyclic peptides. The peptide inhibits the agr response,
 CC which is normally associated with the release of virulence factors of
 CC Staphylococcus aureus. An AgrD peptide is produced by *S. aureus* that

CC activates the agr response in strains of a single group, but interferes
 CC with this response in strains of different groups. The peptides and
 CC composition containing them can be used to treat infections by *S. aureus*
 XX Sequence 9 AA;

Query Match 87.2%; Score 34; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXASLIF 9

DB 1 GVNAXSSSLF 9

RESULT 12

AAV67861

ID AAV67861 standard; peptide; 9 AA.

XX AC AAV67861;

XX DT 25-APR-2000 (first entry)

XX DE Staphylococcus aureus AgrDII derived peptide sequence.

XX KW Staphylococcus aureus infection; AgrD; agr response; treatment;
 KW virulence factor.

XX OS Staphylococcus aureus.

XX FH Key Location/Qualifiers

FT Misc-difference 5 /label= Unknown

XX WO9967286-A2.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-US014562.

XX PR 24-JUN-1998; 98US-00103438.

XX PA (UYRQ) UNIV ROCKEFELLER.

XX PA (UUNY) UNIV NEW YORK STATE.

XX PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX DR WPI; 2000-147202/13.

XX PT New cyclic peptides for treating infections with Staphylococcus aureus.

XX PS Example; Page 22; 37pp; English.

XX This sequence represents the Staphylococcus aureus AgrDII derived
 CC peptide. The invention relates to AgrD derived cyclic peptides, a
 CC composition containing a peptide and a carrier, and a method for the
 CC production of the cyclic peptides. The peptide inhibits the agr response,
 CC which is normally associated with the release of virulence factors of
 CC Staphylococcus aureus. An AgrD peptide is produced by *S. aureus* that
 CC activates the agr response in strains of a single group, but interferes
 CC with this response in strains of different groups. The peptides and
 CC composition containing them can be used to treat infections by *S. aureus*

Sequence 9 AA;

Query Match 87.2%; Score 34; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXASLIF 9

DB 1 GVNAXSSSLF 9

RESULT 13
 ABB07161
 ID ABB07161 standard; peptide; 9 AA.
 XX
 AC ABB07161;
 XX
 DT 13-MAR-2002 (first entry)
 XX
 DE Peptide-mediated quorum sensing inhibitor peptide cyclo-XIII.
 XX
 KW Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
 KW vulnary; pheromone; agr system; accessory gene regulator; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 5 /note= "diaminopropionic acid residue"
 FT
 XX WO200185664-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 10-MAY-2001; 2001WO-US015221.
 XX
 XX 10-MAY-2000; 2000US-0203000P.
 PR 07-DEC-2000; 2000US-0254398P.
 XX
 XX (UYP-) UNIV PRINCETON.
 PA (QUOR-) QUOREX PHARM INC.
 PA (UYTE-) UNIV TECHNOLOGIES INT INC.
 XX
 PI Bassler BL, Dammel CS, Schauder S, Shokat K, Stein J, Surette MG;
 XX
 DR WPI; 2002-075235/10.
 XX
 XX Use of autoinducer-2 agonists or antagonists for regulating activity of
 PT autoinducer-2 receptor, regulating bacterial growth and pathogenesis,
 PT also antibiotic compositions.
 XX
 PS Disclosure; Page 33; 134pp; English.
 XX
 CC The invention relates to the use of autoinducer-2 (AI-2) agonists or
 CC antagonists for regulating activity of autoinducer-2 receptor, regulating
 CC bacterial growth and pathogenesis. Synergistic antibiotic compositions
 CC comprising inhibitors of the quorum-sensing pathway of a microorganism
 CC are also provided. Methods using such AI-2 analogues are useful for
 CC treating pathogen-associated disease states. The compounds and/or biofilm
 CC compositions can be used to inhibit bacterial cell growth and/or biofilm
 CC formation on a medical device, particularly for promoting growth of skin
 CC graft replacements used in the treatment of burns and ulcers. They may
 CC also be used to aid wound repair, and to inhibit bacterial cell growth
 CC and biofilm formation in or on products or devices used for personal
 CC hygiene. The present sequence represents an inhibitor of peptide-mediated
 CC quorum sensing
 XX
 SQ Sequence 9 AA;

Query Match 87.2%; Score 34; DB 5; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVNAXSLF 9
 |||||:
 Db 1 GVNAXSLF 9

RESULT 14
 AAM51005
 ID AAM51005 standard; peptide; 9 AA.
 XX
 AC AAM51005;

Sequence 9 AA;

Query Match 87.2%; Score 34; DB 5; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVNAXSLF 9
 |||||:
 Db 1 GVNAXSLF 9

RESULT 15
 AAM50908
 ID AAM50908 standard; peptide; 9 AA.

XX 07-AUG-2003 (revised)
 DT 08-MAY-2002 (first entry)
 XX
 DE AgrD2 lactam cyclic peptide.
 XX
 KW AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
 KW therapy; cyclic.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"
 FT Misc-difference 5 /note= "any amino acid"
 FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"
 FT
 XX US6337385-B1.
 XX
 XX 08-JAN-2002.
 XX
 XX 24-JUN-1999; 99US-00339511.
 XX
 XX 24-JUN-1998; 98US-0090402P.
 PR (UYEQ) UNIV ROCKEFELLER.
 PA (UYNY) UNIV NEW YORK STATE.
 XX
 PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
 XX
 DR WPI; 2002-170774/22.
 XX
 XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 PT interference and for treating Staphylococcus aureus infection in a
 PT subject.
 XX
 PS Example 1; Col 11; 18pp; English.
 XX

CC The present sequence is that of a novel synthetic AgrD2 lactam cyclic
 CC peptide in which residue 5 of the peptide is linked to residue 9 via a
 CC lactam bond. The peptide is derived from an AgrD2 peptide of
 CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
 CC where the agr locus controls the synthesis of virulence factor and other
 CC extracellular proteins responsible for pathogenicity in *S. aureus*. The
 CC biological activity of the synthetic peptide was assayed using cultured
 CC *S. aureus* strains containing a beta-lactamase reporter gene fused to the
 CC agrp3 promoter. This allowed activation or inhibition of the agr response
 CC to be monitored spectrophotometrically. The AgrD3 lactam peptide
 CC inhibited the agr response in group I *S. aureus* strains and did not
 CC activate the agr response in group I, II or III strains. The invention
 CC provides claimed cyclic peptides (see AAM50899-906 and AAM50999) and
 CC methods for preparing them, especially where the cyclic bond is a lactam
 CC or lactone bond. The cyclic peptides are useful for bacterial
 CC interference, especially for the treatment of *S. aureus* infection.
 CC (Updated on 07-AUG-2003 to correct OS field.)
 XX

XX AC AAM50908;
 XX DT 08-MAY-2002 (first entry)
 XX DE Protected peptide used in cyclic peptide production.
 XX KW Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
 XX KW antibacterial; infection; therapy; cyclic.
 XX OS Synthetic.
 XX FH
 XX FT
 XX FT Location/Qualifiers
 XX FT Modified-site 1
 XX FT /note= "Z-Gly"
 XX FT Misc-difference 5
 XX FT /note= "note linked to residue 9 to form cyclic peptide"
 XX FT Modified-site 5
 XX FT /label= Dpr(Boc)
 XX FT Modified-site 6
 XX FT /note= "Ser(Bzl)"
 XX FT Modified-site 7
 XX FT /note= "Ser(Bzl)"
 XX FT Misc-difference 9
 XX FT /note= "note linked to residue 5 to form cyclic peptide"
 XX FT
 XX PN US6337385-B1.
 XX XX
 XX PD 08-JAN-2002.
 XX XX
 XX PF 24-JUN-1999; 99US-00339511.
 XX XX
 XX PR 24-JUN-1998; 98US-0090402P.
 XX XX
 XX PA (UYRO) UNIV ROCKEFELLER.
 XX PA (UYN) UNIV NEW YORK STATE.
 XX FI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
 XX DR WPI; 2002-170774/22.
 XX XX
 XX PT Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 XX FT interference and for treating Staphylococcus aureus infection in a
 XX FT subject.
 XX PS Disclosure; Col 14; 18pp; English.
 XX CC
 XX CC The present sequence is that of a protected peptide used in an example of
 XX CC the preparation of novel synthetic cyclic peptides of the invention (see
 XX CC AAM50899-906). The peptide corresponds to the Staphylococcus aureus
 XX CC AgrDII sequence with a Cys to diaminopropionic acid (Dpr) mutation
 XX CC (lactam). It was synthesised on a Wang-resin using an Fmoc N-alpha
 XX CC protection strategy. Following chain assembly, the peptide was cleaved
 XX CC from the support and the Dpr-5 residue deprotected by treatment with a
 XX CC trifluoroacetic acid:anisole:water mixture (90:5:5) for 4 hr. The
 XX CC partially protected peptide-alpha carboxylates were then dissolved in DMF
 XX CC and treated with PyBOP. Cyclization was complete after 2 hr. The
 XX CC remaining protecting groups were removed by treatment with HF and the
 XX CC peptide purified by HPLC. The cyclic peptide is capable of inhibiting the
 XX CC agr response of Staphylococcus aureus. The thiolactone structure within
 XX CC native AgrD peptides is required for activation of this response.
 XX CC Replacement of the thiol ester component of the cyclic ring structure
 XX CC with a lactam (as in the present case) or a lactone can destroy agr
 XX CC response activating activity while preserving and enhancing inhibitory
 XX CC activity. The cyclic peptides are useful for bacterial interference,
 XX CC especially for the treatment of S. aureus infection
 XX SQ Sequence 9 AA;

Query Match 87.2%; Score 34; DB 5; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVNAXASLF 9
 |||||:
 Db 1 GVNAXSSLF 9

Search completed: October 26, 2004, 15:59:44
 Job time : 44.75 secs

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:54:00 ; Search time 31.5 Seconds
(without alignments)
92.502 Million cell updates/sec

Title: US-10-032-950-5
Perfect score: 39
Sequence: 1 GVNAXASLF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA.*
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 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	94.9	9	13	US-10-032-950-5
2	34	87.2	9	13	Sequence 5, Appli
3	33	84.6	9	14	Sequence 1, Appli
4	33	84.6	47	14	Sequence 3, Appli
5	32	82.1	271	15	Sequence 6, Appli
6	32	82.1	294	16	Sequence 72245, A
7	32	82.1	490	14	Sequence 40441, A
8	31	79.5	9	13	US-10-032-950-5
9	31	79.5	279	14	Sequence 6, Appli
10	31	79.5	800	14	Sequence 11888, A
11	30	76.9	9	13	Sequence 14064, A
12	30	76.9	147	11	Sequence 2, Appli
13	30	76.9	340	15	Sequence 7334, Ap
					Sequence 53320, A

14	30	76.9	347	15	US-10-282-122A-52679	Sequence 52679, A
15	30	76.9	396	15	US-10-282-122A-63115	Sequence 63115, A
16	30	76.9	415	14	US-10-292-798-1638	Sequence 1638, Ap
17	30	76.9	432	14	US-10-017-161-2252	Sequence 2252, Ap
18	30	76.9	432	14	US-10-292-798-1898	Sequence 1898, Ap
19	30	76.9	572	15	US-10-282-122A-78027	Sequence 78027, A
20	30	76.9	1203	16	US-10-437-963-120758	Sequence 120758, A
21	30	76.9	1804	16	US-10-437-963-111282	Sequence 111282, A
22	29	74.4	9	13	US-10-032-950-7	Sequence 7, Appli
23	29	74.4	147	16	US-10-437-963-197826	Sequence 197826, A
24	29	74.4	266	16	US-10-767-701-40852	Sequence 40852, A
25	29	74.4	317	15	US-10-282-122A-48025	Sequence 48025, A
26	29	74.4	332	14	US-10-145-586-46	Sequence 46, Appli
27	29	74.4	468	14	US-10-369-493-12194	Sequence 12194, A
28	29	74.4	488	10	US-09-826-509-561	Sequence 561, App
29	29	74.4	488	14	US-10-225-567A-296	Sequence 296, App
30	29	74.4	488	14	US-10-320-351-3	Sequence 3, Appli
31	29	74.4	488	14	US-10-295-027-1326	Sequence 1326, Ap
32	29	74.4	488	16	US-10-755-889-170	Sequence 170, App
33	29	74.4	513	15	US-10-425-114-71814	Sequence 71814, A
34	29	74.4	515	15	US-10-424-599-246184	Sequence 246184, A
35	29	74.4	605	9	US-09-841-132-574	Sequence 574, App
36	29	74.4	747	9	US-09-978-295A-459	Sequence 459, App
37	29	74.4	747	9	US-09-938-418-9	Sequence 9, Appli
38	29	74.4	747	9	US-09-978-697-459	Sequence 459, App
39	29	74.4	747	9	US-09-978-192A-459	Sequence 459, App
40	29	74.4	747	9	US-09-999-832A-459	Sequence 459, App
41	29	74.4	747	10	US-09-978-189-459	Sequence 459, App
42	29	74.4	747	10	US-09-978-608A-459	Sequence 459, App
43	29	74.4	747	10	US-09-978-585A-459	Sequence 459, App
44	29	74.4	747	10	US-09-978-191A-459	Sequence 459, App
45	29	74.4	747	10	US-09-978-403A-459	Sequence 459, App

ALIGNMENTS

RESULT 1

US-10-032-950-5
; Sequence 5, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Vuir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; FILE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-5

Query Match 94.9%; Score 37; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVNAXASLF 9

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Db      1  GVNAXASLRF 9
|||||
RESULT 2
US-10-032-950-1
; Sequence 1, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-1
Query Match      87.2%; Score 34; DB 13; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GVNAXASLRF 9
|||||
Db      1  GVNAXSSLF 9
|||||
RESULT 3
US-10-201-444-3
; Sequence 3, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT APPLICATION NUMBER: US/10/201,444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-3
Query Match      84.6%; Score 33; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches      7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GVNAXASLRF 9
|||||
Db      1  GVNACSSLF 9
|||||
RESULT 4
US-10-201-444-6
; Sequence 6, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT APPLICATION NUMBER: US/10/201,444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-6
Query Match      84.6%; Score 33; DB 14; Length 47;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches      7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GVNAXASLRF 9
|||||
Db      24  GVNACSSLF 32
|||||
RESULT 5
US-10-282-122A-72245
; Sequence 72245, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 72245
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-282-122A-72245

Query Match      82.1%; Score 32; DB 15; Length 271;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXASLF 9
Db 120 GVNPFASLF 128

RESULT 6
US-10-767-701-40441
; Sequence 40441, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 40441
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(294)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C60451_1.pep
US-10-767-701-40441

Query Match      82.1%; Score 32; DB 16; Length 294;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXASLF 9
Db 255 GLNSTASLF 263

RESULT 7
US-10-243-351-2
; Sequence 2, Application US/10243351
; Publication No. US20030059890A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven
; TITLE OF INVENTION: DNA ENCODING THE CHIMPANZEE PROTAGLANDIN E2 RECEPTOR EP4 SUBTYPE
; FILE REFERENCE: PCL1827AGR
; CURRENT APPLICATION NUMBER: US/10/243,351
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/322,915
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 490
; TYPE: PRT
; ORGANISM: chimpanzee
US-10-243-351-2

; SEQ ID NO 72245
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-282-122A-72245

Query Match      82.1%; Score 32; DB 14; Length 490;
Best Local Similarity 87.5%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXASL 8
Db 5 GVNASASL 12

RESULT 8
US-10-032-950-6
; Sequence 6, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-6

Query Match      79.5%; Score 31; DB 13; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXASLF 9
Db 1 GVNAXASLF 9

RESULT 9
US-10-369-493-11888
; Sequence 11888, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11888
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-369-493-11888
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Query Match 79.5%; Score 31; DB 14; Length 279;
 Best Local Similarity 87.5%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXASL 8
 |||||
 DB 139 GVNAFASL 146

RESULT 10

US-10-369-493-14064
 ; Sequence 14064, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 14064
 ; LENGTH: 800
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas fluorescens
 US-10-369-493-14064

Query Match 79.5%; Score 31; DB 14; Length 800;
 Best Local Similarity 77.8%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps, 0;

QY 1 GVNAXASL 9
 |||||
 DB 133 GVTALASL 141

RESULT 11

US-10-032-950-2
 ; Sequence 2, Application US/10032950
 ; Publication No. US20020077453A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Muir, Tom
 ; APPLICANT: Mayville, Patricia
 ; APPLICANT: No. US20020077453A1, Richard P.
 ; APPLICANT: Beavis, Ronald
 ; APPLICANT: Ji, Guangyong
 ; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
 ; FILE REFERENCE: 600-1-231N
 ; CURRENT APPLICATION NUMBER: US/10/032,950
 ; CURRENT FILING DATE: 2001-12-27
 ; PRIOR FILING DATE: 2001-12-27
 ; PRIOR FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; NAME/KEY: VARIANT
 ; LOCATION: (5)
 ; OTHER INFORMATION: Xaa represents any amino acid at this position.
 US-10-032-950-2

Query Match 76.9%; Score 30; DB 13; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.2e+06;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXASL 9
 |||||
 DB 1 GANAXSSL 9

RESULT 12

US-09-864-408A-7334
 ; Sequence 7334, Application US/09864408A
 ; Publication No. US20040009474A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leach, Martin D.
 ; APPLICANT: Shimkets, Richard A.
 ; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Enco
 ; FILE REFERENCE: 21402-012
 ; CURRENT APPLICATION NUMBER: US/09/864,408A
 ; CURRENT FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: 60/206,690
 ; PRIOR FILING DATE: 2000-05-24
 ; NUMBER OF SEQ ID NOS: 9068
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7334
 ; LENGTH: 147
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
 US-09-864-408A-7334

Query Match 76.9%; Score 30; DB 11; Length 147;
 Best Local Similarity 66.7%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXASL 9
 |||||
 DB 41 GINLPASL 49

RESULT 13

US-10-282-122A-53320
 ; Sequence 53320, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Chlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06

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/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 53320
/ LENGTH: 340
/ TYPE: PRT
/ ORGANISM: Clostridium difficile
US-10-282-122A-53320

Query Match.          76.9%; Score 30; DB 15; Length 340;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GVNAXASLF 9
      |:|:|:|:|
Db      98 GINSGAALF 106

RESULT 14
US-10-282-122A-52679
/ Sequence 52679, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 53320
/ LENGTH: 396
/ TYPE: PRT
/ ORGANISM: Moraxella catarrhalis
US-10-282-122A-63115

Query Match          76.9%; Score 30; DB 15; Length 396;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GVNAXASLF 9
      |:|:|:|:|
Db      230 GVNUGASLF 238

RESULT 15
US-10-282-122A-63115
/ Sequence 63115, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 63115
/ LENGTH: 396
/ TYPE: PRT
/ ORGANISM: Moraxella catarrhalis
US-10-282-122A-63115

Query Match          76.9%; Score 30; DB 15; Length 396;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GVNAXASLF 9
      |:|:|:|:|
Db      230 GVNUGASLF 238
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Wed Oct 27 09:38:13 2004

us-10-032-950-5.rapb

Page 6

Search completed: October 26, 2004, 16:10:12
Job time : 31.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:46:55 ; Search time 8.73529 Seconds
(without alignments)
99.132 Million cell updates/sec

Title: US-10-032-950-5

Perfect score: 39

Sequence: 1 GVNAXASLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	94.9	333	1 C69812	ferrichrome ABC tr
2	33	84.6	47	2 C89995	AgrD protein [impo
3	32	82.1	382	2 A28067	lysosomal membrane
4	32	82.1	405	2 A60534	P2B/LAMP-1 precurs
5	32	82.1	407	2 A30200	120K lysosomal mem
6	31	79.5	349	2 S74439	iron(III) dicitrat
7	31	79.5	468	2 T24523	hypothetical prote
8	30	76.9	188	2 B38116	hypothetical prote
9	30	76.9	188	2 AC2563	transposase alf850
10	30	76.9	234	2 S60895	ferric exochelin u
11	30	76.9	247	2 AG2524	transposase alf1737
12	30	76.9	247	2 A12490	transposase alf1710
13	30	76.9	247	2 AG2491	transposase alf1711
14	30	76.9	247	2 AD2478	transposase alf1700
15	30	76.9	247	2 A12499	transposase alf1717
16	30	76.9	247	2 AF2515	transposase alf1730
17	30	76.9	259	2 T11068	cytochrome-c oxida
18	30	76.9	346	2 AB2129	iron(III) dicitrat
19	30	76.9	361	2 AD3198	hypothetical prote
20	30	76.9	458	2 A83391	probable glutamine
21	30	76.9	458	2 B83609	probable glutamine
22	30	76.9	497	2 AC2518	transposase alf732
23	30	76.9	497	2 AC2518	transposase alf732
24	30	76.9	497	2 AD2511	transposase alf1726
25	30	76.9	572	2 AC0325	urease (EC 3.5.1.5
26	30	76.9	573	2 S36028	urease (EC 3.5.1.5
27	30	76.9	649	2 P83779	iron (III) dicitra
28	30	76.9	1232	2 T06165	multidrug resistan
29	29	74.4	109	2 A99227	hypothetical prote

30	29	74.4	148	2 D97308	probable membrane
31	29	74.4	488	2 A53572	prostaglandin E2 r
32	29	74.4	500	1 EPEF	zip protein precur
33	29	74.4	570	2 T33320	hypothetical prote
34	29	74.4	605	2 H1562	probable flagellar
35	29	74.4	655	2 G89189	protein Y32F6A.3 [
36	29	74.4	703	2 T41065	RNA binding protein
37	29	74.4	895	2 T45786	receptor-protein k
38	29	74.4	1238	2 T40120	C2H2 type zinc fin
39	28	71.8	186	2 D83354	hypothetical prote
40	28	71.8	255	2 AD1159	flagellar biosynth
41	28	71.8	255	2 AD1518	flagellar biosynth
42	28	71.8	297	2 E83194	polysamine transpor
43	28	71.8	333	2 D69805	iron(III) dicitrat
44	28	71.8	369	2 A4942	fructose-bisphosph
45	28	71.8	369	2 B43715	protein M homolog

ALIGNMENTS

RESULT 1

C69812
ferrichrome ABC transporter (permease) homolog yfmd - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: C69812
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galle
techt, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y, M.; Ogasawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seto
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsara, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: C69812
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-333 <KUN>
A/Cross-references: UNIPROT:O34933; GB:Z99108; GB:AL009126; NID:G2633055; PIDN:CAB12580
A/Experimental source: strain 168
C/Genetics:
A/Gene: yfmd
C/Superfamily: ferrichrome ABC transporter

Query Match 94.9%; Score 37; DB 1; Length 333;
Best Local Similarity 88.9%; Pred. No. 0.53;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXASLF 9

Db 99 GVNAGASLF 107

RESULT 2

C89995
AgrD protein [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: C89995
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:213111952; PMID:11418146
 A:Accession: C89995
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-47 <KUR>
 A:Cross-references: UNIPROT:Q33586; GB:BA000018; PID:gl3701831; PIDN:BA43124.1; GSPDB:G
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: agrD

Query Match 84.6%; Score 33; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 0.61;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASLIF 9
 ||||| :|||
 Db 24 GVNACSSLIF 32

RESULT 3

A28067 lysosomal membrane glycoprotein LAMP-1 - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
 C:Accession: A28067
 R:Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T.
 J. Biol. Chem. 263, 8754-8758, 1988

A:Title: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprotein
 A:Reference number: A28067; MUID:88243732; PMID:3379044
 A:Accession: A28067
 A:Molecule type: mRNA

A:Residues: 1-382 <CHE>
 A:Cross-references: UNIPROT:P11438; GB:J03881; NID:G198706; PIDN:AAA39411.1; PID:G293692

A:Note: the authors translated the codon ATT for residue 1 as Leu and CCG for residue 2
 C:Superfamily: lysosome-associated membrane protein
 C:Keywords: glycoprotein; membrane protein

Query Match 82.1%; Score 32; DB 2; Length 382;
 Best Local Similarity 66.7%; Pred. No. 9.9;
 Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

Qy 1 GVNAXASLIF 9
 ||||| :|||
 Db 256 GVNASSLIF 264

RESULT 4

A60534 P2B/LAMP-1 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C:Accession: A60534

R:Heffernan, M.; Yousefi, S.; Dennis, J.W.

Cancer Res. 49, 6077-6084, 1989

A:Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastasi

A:Reference number: A60534; MUID:90020989; PMID:2676155

A:Accession: A60534

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-405 <HEF>

A:Cross-references: UNIPROT:P11438

C:Superfamily: lysosome-associated membrane protein

Query Match 82.1%; Score 32; DB 2; Length 405;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASLIF 9
 ||||| :|||
 Db 279 GVNASSLIF 287

RESULT 5

A30200 120K lysosomal membrane glycoprotein precursor - rat
 N:Alternate names: sialoglycoprotein
 A:Species: Rattus norvegicus (Norway rat)
 C:Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: A30200; S03331
 R:Howe, C.L.; Granger, B.L.; Hull, M.; Green, S.A.; Gabel, C.A.; Helenius, A.; Mellman, Proc. Natl. Acad. Sci. U.S.A. 85, 7577-7581, 1988
 A:Title: Derived protein sequence, oligosaccharides, and membrane insertion of the 120-k glycoproteins.

A:Reference number: A30200; MUID:89017240; PMID:3174652

A:Accession: A30200

A:Molecule type: mRNA

A:Residues: 1-407 <HOW>

A:Cross-references: UNIPROT:P14562; EMBL:J03672

A:Note: the authors translated the codon GGG for residue 15 as Val

R:Himeno, M.; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, K.; Kono, A.; Sakaki, Y.; Kat FEBS Lett. 244, 351-356, 1989

A:Title: Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in
 A:Reference number: S03331; MUID:89153580; PMID:2920835

A:Accession: S03331

A:Molecule type: mRNA

A:Residues: 22-407 <HIM>

A:Cross-references: EMBL:X14765; NID:G56577; PIDN:CAA32873.1; PID:G56578

A:Note: part of this sequence, including the amino end of the mature protein, was confir

C:Superfamily: lysosome-associated membrane protein

C:Keywords: glycoprotein; membrane protein

F122-407/Product: lysosomal membrane glycoprotein, 107K #status experimental <MAT>

Query Match 82.1%; Score 32; DB 2; Length 407;

Best Local Similarity 66.7%; Pred. No. 11;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASLIF 9
 ||||| :|||
 Db 281 GVNATSSLIF 289

RESULT 6

S74439

iron(III) dicitrate transport system permease protein fecD - Synechocystis sp. (strain P

N:Alternate names: protein sir317

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S74439

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

C:K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

s.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74439

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-349 <KAN>

A:Cross-references: UNIPROT:P72591; EMBL:D90899; GB:AB001339; NID:gl651650; PIDN:BAAL1659

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: fecD

C:Superfamily: vitamin B12 transport protein btuC

C:Keywords: iron transport

Query Match 79.5%; Score 31; DB 2; Length 349;

Best Local Similarity 87.5%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASLIF 8
 ||||| :|||
 Db 113 GVNAGASLIF 120

RESULT 7

T24523
hypothetical protein T05E11.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24523
R:Kershaw, J.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z19903
A:Accession: T24523
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-468 <WIL>
A:Cross-references: UNIPROT:P49049; EMBL:Z68751; PIDN:CRA92975.1; GSPDB:GN00022; CBSP:TO
A:Experimental source: clone T05E11
C:Genetics:
A:Gene: CBSP:T05E11.5
A:Map position: 4
A:Introns: 23/3; 293/3

Query Match 79.5%; Score 31; DB 2; Length 468;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASL 8
||| |||
Db 181 GVNAFASL 188

RESULT 8
B38116
hypothetical protein 2 - Anabaena sp. insertion sequence IS892 -
C:Species: Anabaena sp.
C>Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004
C:Accession: B38116
R:Ca, Y.
J. Bacteriol. 173, 5771-5777, 1991
A:Title: Characterization of insertion sequence IS892 and related elements from the cyan
A:Reference number: A38116; MUID:91358369; PMID:1653218
A:Accession: B38116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <CAI>
A:Cross-references: UNIPROT:Q8YK27; GB:M64297
A:Experimental source: PCC 7120
C:Genetics:
A:Mobile element: insertion sequence IS892
C:Superfamily: Anabaena insertion sequence IS892 hypothetical protein 2

Query Match 76.9%; Score 30; DB 2; Length 188;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASL 9
||| |||
Db 5 GLSATASL 13

RESULT 9
AC2563
transposase alr-8502 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120delta
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC2563
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2563
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <KUR>

A:Cross-references: UNIPROT:Q8YK27; GB:AF003604; PIDN:BAW7421.1; PID:gl7134865; GSPDB:Q
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr8502
A:Superfamily: Anabaena insertion sequence IS892 hypothetical protein 2

Query Match 76.9%; Score 30; DB 2; Length 188;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASL 9
||| |||
Db 5 GLSATASL 13

RESULT 10
S60885
ferric exochelin uptake protein fxuC - Mycobacterium smegmatis (fragment)
C:Species: Mycobacterium smegmatis
C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S60885
R:Fiss, E.H.; Yu, S.; Jacobs Jr., W.R.
Mol. Microbiol. 14, 557-569, 1994
A:Title: Identification of genes involved in the sequestration of iron in mycobacteria:
A:Reference number: S60885; MUID:95191405; PMID:7885234
A:Accession: S60885
A:Molecule type: DNA
A:Residues: 1-234 <FIS>
A:Cross-references: UNIPROT:Q50375; EMBL:U10425; NID:G595400; PIDN:AAC43258.1; PID:G595
C:Genetics:
A:Gene: fxuC

Query Match 76.9%; Score 30; DB 2; Length 234;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASL 9
||| |||
Db 37 GLSGAALF 45

RESULT 11
AG2524
transposase all7375 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AG2524
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2524
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <KUR>
A:Cross-references: UNIPROT:Q8YK25; GB:BA000020; PIDN:BAW77133.1; PID:gl7134574; GSPDB:
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all7375
A:Superfamily: Anabaena insertion sequence IS892 hypothetical protein 2

Query Match 76.9%; Score 30; DB 2; Length 247;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASL 9
||| |||
Db 64 GLSATASL 72

RESULT 12
AI2490
transposase all7105 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AI2490
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AI2490
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <KUR>
A:Cross-references: UNIPROT:Q8XGA1; GB:BA000020; PIDN:BA878189.1; PID:gl7135643; GSPDB:C
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all7105
A:Genome: plasmid
C:Superfamily: Anabaena insertion sequence IS892 hypothetical protein 2

```

Query Match          76.9%; Score 30; DB 2; Length 247;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  GVNAXASLFF 9
      |.:|:|:|
Db       64  GLSATASLFF 72

RESULT 13
AG2491
transposase all7111 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;accession: AG2491
R;kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840

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A/Molecule type: DNA
A/Accession: F01222
A/Residues: 1-247 <KUR>
A/Cross-references: UNIPROT:Q8XGAL; GB:BA000020; PIDN:BA878195.1; PID:gl7135649; GSPDB:G
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: all7111
A/Genome: plasmid
C/Superfamily: Anabaena insertion sequence IS992 hypothetical protein 2

Query Match          76.9%; Score 30; DB 2; Length 247;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  GVNAXASLP 9
Db      64  GUSATASLP 72
          ||::|||
          ||::|||

RESULT 14
AD2478
transposase all7004 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
C/Species: Nostoc sp. PCC 7120
A/Name: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AD2478
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriouchi

```

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 2005-213, 2001
 A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
 A; Reference number: AB1807; MUID:21595285; PMID:11759840
 A; Accession: AD2478
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-247 <XUR>
 A; Cross-references: UNIPROT:G6XG1; GB:BA000020; PIDN:BA8088.1; PID:g17135542; GSPDB:C
 A; Experimental source: strain PCC 7120
 C; Genetics:
 A; Gene: all7004
 A; Genome: plasmid
 C; Superfamily: Anabaena insertion sequence IS892 hypothetical protein 2

```

Query Match          76.9%; Score 30; DB 2; Length 247;
Best Local Similarity 56.7%; Pred. NO. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GYNVXASL 9
      ||::|||
Db      64 GUSATASL 72

RESULT 15
AI2499
C:Species: Nostoc sp. PCC 7120
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AI2499
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AI2499
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <KUR>
A:Cross-references: UNIPROT:Q8XGAL; GB:BA000020; PIDN:BA078261.1; PTD:G171335715; GSPDB:G171335715
A:Experimental source: strain PCC 7120

```

A: genome: plasmid
 C: Superfamily: Anabaena insertion sequence rs892 hypothetical protein 2
 Query Match 76.9%; Score 30; DB 2; Length 247;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GVNAXASLF 9
 : : : : :
 Db 64 GLSATASLF 72

Search completed: October 26, 2004, 16:06:09
Job time : 9.73529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:50 ; Search time 40.6324 Seconds
(without alignments)
127.445 Million cell updates/sec

Title: US-10-032-950-5

Perfect score: 39

Sequence: 1 GVNAXASLF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	94.9	333	2	O34933
2	33	84.6	47	2	O33586
3	33	84.6	47	2	O7A2N4
4	33	84.6	47	2	O7A4I7
5	33	84.6	47	2	CAE92745
6	33	84.6	47	2	CAE92748
7	33	84.6	47	2	CAE92751
8	33	84.6	47	2	CAE92754
9	33	84.6	47	2	CAE92757
10	33	84.6	153	2	O89EV1
11	33	84.6	463	2	O8XHH9
12	32	82.1	189	2	O92T19
13	32	82.1	259	2	O8HNS0
14	32	82.1	263	2	O6ZM65
15	32	82.1	263	2	CAE50608
16	32	82.1	271	1	OXAL_STRMU
17	32	82.1	406	1	LMP1_MOUSE
18	32	82.1	406	2	O8VH34
19	32	82.1	407	1	LMP1_RAT
20	32	82.1	407	2	O9DC13
21	32	82.1	490	1	PE24_PANTR
22	32	82.1	1248	2	O9M838
23	31	79.5	259	2	O70US2
24	31	79.5	259	2	CAD61194
25	31	79.5	279	2	O98X81
26	31	79.5	349	2	F72591
27	31	79.5	468	1	XJ95_CAEEL
28	31	79.5	578	2	O9PKY0
29	31	79.5	885	2	O876F4
30	31	79.5	906	2	O6FWD3
31	31	79.5	1959	2	O70C52

RESULT 1

O34933 PRELIMINARY; PRT; 333 AA.
AC O34933; Q79ET2;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-OCT-2004 (TREMELrel. 28, Last annotation update)
DE Yfmb Protein.
GN Name-yfmd; OrderedLocusNames=BSU07510;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]_TaxID=1423;
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=980404033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertoletti M.G., Bessieres P., Bolotin A., Borchert S.,
RA Bortiss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.P., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein M., Kurita K., Lapidus A., Koningsstein G., Krohn S.,
RA Kumano M., Kurita K., Lapidus A., Mizuno M., Moestl D., Nakai S.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Maue C.,
RA Medigue C., Medina N., Mellado R.P., Lardinois S., Lauber J.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Pressac E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.S., Solido B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitznegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis";
RL Nature 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AC327;
RX MEDLINE=97417488; PubMed=9272861;
RA Yamamoto H., Uchiyama S., Nigroho F.A., Sekiguchi J.;
RT "Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region

ALIGNMENTS

32 31 79.5 1959 2 CAE52334 xanthomon
33 30 76.9 63 2 Q9RCK4 streptococ
34 30 76.9 188 2 Q8YK27 anabaena sp
35 30 76.9 234 2 Q50375 mycobacteri
36 30 76.9 242 2 Q94U25 leishmania
37 30 76.9 247 2 Q8XGAL anabaena sp
38 30 76.9 247 2 Q8YKCS anabaena sp
39 30 76.9 255 2 Q78BR1 carassius a
40 30 76.9 255 2 Q98SE3 carassius a
41 30 76.9 259 2 O47576 onchocerca
42 30 76.9 300 2 Q737N6 bacillus ce
43 30 76.9 300 2 A8A41526 bacillus
44 30 76.9 303 2 Q8HIC7 bacillus th
45 30 76.9 337 2 Q8XM78 clostridium

RT of the *Bacillus subtilis* genome reveal genes for a new two-component
 RT system, three spore germination proteins, an iron uptake system and a
 RT general stress response protein.";

RL Gene 194:191-199(1997).
 DR EMBL: Z99108; CAB12580.1; -;
 DR EMBL: D86417; BAA22318.1; -;
 DR FTR: C69812; C69812.

DR HSP: P08609; ILTV.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005215; P:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.

DR InterPro: IPR00522; FecD.
 DR Pfam: PF01032; FecCD; 1.
 DR Complete proteome.

SW SEQUENCE 333 AA; 35098 MW; 9F4BE91BB0EE6761 CRC64;

Query Match 94.9%; Score 37; DB 2; Length 333;
 Best Local Similarity 88.9%; Pred. No. 3.6;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASLFP 9
 |||||
 Db 99 GVNAGASLFP 107

RESULT 2
 O33586 PRELIMINARY; PRT; 47 AA.

ID O33586
 AC O33586
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE AgrD.

GN Name=agrD;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=1280;
 RN [1]
 RC STRAIN=SA502A;
 RC MEDLINE=97342847; PubMed=9197262;

RA Ji G., Beavis R., Novick R.P.;
 RA "Bacterial interference caused by autoinducing peptide variants.";
 RL Science 276:2027-2030(1997).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Gt31a-cp5, Gt31b-cp5, Gt31c-cp8, Gt31d-cp8, and Gt111-cp8;

RA Goerke C., Dabach S., Kuemmel M., Wolz C.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF001782; AAB63265.1; -;
 DR EMBL: AJ617715; CAE92748.1; -;
 DR EMBL: AJ617716; CAE92748.1; -;

DR EMBL: AJ617717; CAE92751.1; -;
 DR EMBL: AJ617718; CAE92754.1; -;
 DR EMBL: AJ617719; CAE92757.1; -;

DR FTR: C89995; C89995.
 DR InterPro: IPR009229; AgrD.
 DR Pfam: PF05931; AgrD; 1.

SW SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
 Query Match 84.6%; Score 33; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 4.2;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASLFP 9
 |||||
 Db 24 GVNACSSLFP 32

RESULT 3
 Q7A2N4 PRELIMINARY; PRT; 47 AA.

ID Q7A2N4
 AC Q7A2N4

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE AgrD protein.

GN Name=agrD; OrderedLocusNames=SAV2037;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.

RC MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Sekimizu K., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";

RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003384; BAB58199.1; -;
 DR InterPro: IPR009229; AgrD.
 DR Pfam: PF05931; AgrD; 1.

DR Complete proteome.
 KW SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 84.6%; Score 33; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 4.2;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASLFP 9
 |||||
 Db 24 GVNACSSLFP 32

RESULT 4
 Q7A4I7 PRELIMINARY; PRT; 47 AA.

ID Q7A4I7
 AC Q7A4I7
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE AgrD protein.

GN Name=agrD; OrderedLocusNames=SA1842.1; ORFNames=SA5066;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.

RC MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Sekimizu K., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";

RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003135; BAB43124.1; -;
 DR InterPro: IPR009229; AgrD.
 DR Pfam: PF05931; AgrD; 1.

DR Complete proteome.
 KW SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 84.6%; Score 33; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 4.2;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXASLFP 9
 |||||
 Db 24 GVNACSSLFP 32

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Db      24 GVNACSSLF 32

RESULT 5
CAE92745
ID      CAE92745      PRELIMINARY;      PRT;      47 AA.
AC      CAE92745;
DT      01-APR-2004 (TRENBLrel. 27, Created)
DT      01-APR-2004 (TRENBLrel. 27, Last sequence update)
DT      01-APR-2004 (TRENBLrel. 27, Last annotation update)
DE      AgrD protein.
GN      AGRD.
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=1280;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=gt31a-cp5;
RA      Goerke C., Dasbach S., Kuemmel M., Wolz C.;
RT      "Evolutionary Models for the Development of the Polymorphic Loci agr
RL      and cap in Staphylococcus aureus.";
RL      Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AJ617715; CAE92745.1;
SQ      SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match      84.6%; Score 33; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GVNAXASLF 9
      ||||:||||
Db      24 GVNACSSLF 32

RESULT 6
CAE92748
ID      CAE92748      PRELIMINARY;      PRT;      47 AA.
AC      CAE92748;
DT      01-APR-2004 (TRENBLrel. 27, Created)
DT      01-APR-2004 (TRENBLrel. 27, Last sequence update)
DT      01-APR-2004 (TRENBLrel. 27, Last annotation update)
DE      AgrD protein.
GN      AGRD.
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=1280;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=gt31b-cp5;
RA      Goerke C., Dasbach S., Kuemmel M., Wolz C.;
RT      "Evolutionary Models for the Development of the Polymorphic Loci agr
RL      and cap in Staphylococcus aureus.";
RL      Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AJ617716; CAE92748.1;
SQ      SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match      84.6%; Score 33; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GVNAXASLF 9
      ||||:||||
Db      24 GVNACSSLF 32

RESULT 7
CAE92751
ID      CAE92751      PRELIMINARY;      PRT;      47 AA.
AC      CAE92751;
DT      01-APR-2004 (TRENBLrel. 27, Created)
DT      01-APR-2004 (TRENBLrel. 27, Last sequence update)
DT      01-APR-2004 (TRENBLrel. 27, Last annotation update)
DE      AgrD protein.

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GN      AGRD.
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=1280;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=gt36a-cp8;
RA      Goerke C., Dasbach S., Kuemmel M., Wolz C.;
RT      "Evolutionary Models for the Development of the Polymorphic Loci agr
RL      and cap in Staphylococcus aureus.";
RL      Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AJ617717; CAE92751.1;
SQ      SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match      84.6%; Score 33; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GVNAXASLF 9
      ||||:||||
Db      24 GVNACSSLF 32

RESULT 8
CAE92754
ID      CAE92754      PRELIMINARY;      PRT;      47 AA.
AC      CAE92754;
DT      01-APR-2004 (TRENBLrel. 27, Created)
DT      01-APR-2004 (TRENBLrel. 27, Last sequence update)
DT      01-APR-2004 (TRENBLrel. 27, Last annotation update)
DE      AgrD protein.
GN      AGRD.
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=1280;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=gt36b-cp8;
RA      Goerke C., Dasbach S., Kuemmel M., Wolz C.;
RT      "Evolutionary Models for the Development of the Polymorphic Loci agr
RL      and cap in Staphylococcus aureus.";
RL      Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AJ617718; CAE92754.1;
SQ      SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match      84.6%; Score 33; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GVNAXASLF 9
      ||||:||||
Db      24 GVNACSSLF 32

RESULT 9
CAE92757
ID      CAE92757      PRELIMINARY;      PRT;      47 AA.
AC      CAE92757;
DT      01-APR-2004 (TRENBLrel. 27, Created)
DT      01-APR-2004 (TRENBLrel. 27, Last sequence update)
DT      01-APR-2004 (TRENBLrel. 27, Last annotation update)
DE      AgrD protein.
GN      AGRD.
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=1280;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=gt111-cp8;
RA      Goerke C., Dasbach S., Kuemmel M., Wolz C.;
RT      "Evolutionary Models for the Development of the Polymorphic Loci agr
RL      and cap in Staphylococcus aureus.";
RL      Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

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DR EMEL; AJ617719; CAE92257.1; --
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
Query Match 84.6%; Score 33; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GVNAXASLIF 9
| | | | | : | | | |
Db 24 GVNACSLF 32
RESULT 10
Q89EVI ID Q89EVI PRELIMINARY; PRT; 153 AA.
AC Q89EVI
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Blr6969 protein.
GN OrderedLocusNames=blr6969;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
EX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMEL; AP005960; BAC52234.1; --
KW Complete proteome.
SQ SEQUENCE 153 AA; 15488 MW; 23C7D464AA94A490 CRC64;
Query Match 84.6%; Score 33; DB 2; Length 153;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GVNAXASLIF 9
| | | | | : | | | |
Db 73 GANAQASLIF 81
RESULT 11
Q8XHH9 ID Q8XHH9 PRELIMINARY; PRT; 463 AA.
AC Q8XHH9
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CPE2505.
GN OrderedLocusNames=CPE2505;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13;
EX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-eater";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMEL; AP003194; BAB82211.1; --
GO: GO:0016020; C:membrane; IEA.

DR GO: GO:0015297; F:antiporter activity; IEA.
DR GO: GO:0015238; F:drug transporter activity; IEA.
DR GO: GO:0006855; P:multidrug transport; IEA.
DR InterPro; IPR002528; MatE.
DR Pfam; PF01554; MatE; 2.
DR TIGRFAMs; TIGR00797; matE; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 463 AA; 51100 MW; 6EE3E385633DEEB9 CRC64;
Query Match 84.6%; Score 33; DB 2; Length 463;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GVNAXASLIF 9
| | | | | : | | | |
Db 65 GINAGASVIF 73
RESULT 12
Q922T9 ID Q922T9 PRELIMINARY; PRT; 189 AA.
AC Q922T9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lamp1 protein (Fragment).
GN Name=Lamp1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZEC II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
EX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshitoki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZEC II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Strausberg R.;
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMEL; BC006785; AAHQ6785.1; --
DR MGD; MGI:96745; Lamp1.
DR GO: GO:0005764; C:lysosome; IEA.
DR GO: GO:0005771; C:multivesicular body; IEA.
DR GO: GO:0042383; C:sarcolemma; IEA.
DR InterPro; IPR002000; Lamp.
DR Pfam; PF01299; Lamp; 1.
DR PRINTS; PR00336; LYSASSOCTDMP.
DR PROSITE; PS00310; LAMP_1; 1.
DR PROSITE; PS00311; LAMP_2; 1.
DR NON_TER 1
FT 1

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SQ SEQUENCE 189 AA; 20456-MW; 71F16D69BA4066FA CRC64;
Query Match 82.1%; Score 32; DB 2; Length 189;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXASLF 9
|:|:|:|:|
Db 63 GVNASSSLF 71

RESULT 13
Q8HN50 PRELIMINARY; PRT; 259 AA.
AC Q8HN50;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit III.
GN Name=cox3;
OS Brugia malayi (Filarial nematode worm).
OG Mitochondrion.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Brugia.
OX NCBI_TaxID=6279;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TR8;
RA Daub J., Mudge J., Blaxter M.L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Subunits I, II and III form the functional core of the
enzyme complex (By similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 3 family.
DR EMBL; AF538716; AA017809.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0016431; F:oxidoreductase activity; IEA.
DR GO; GO:0005118; F:electron transport; IEA.
DR InterPro; IPR000298; CytC_oxdase_III.
DR Pfam; PF00510; COX3; 1.
DR ProDom; PD000382; CytC_oxdase_III; 1.
DR PROSITE; PS0253; COX3_1.
KW Mitochondrion; Oxidoreductase; Transmembrane.
SQ SEQUENCE 259 AA; 30791-MW; 3A8EE64649880596 CRC64;
Query Match 82.1%; Score 32; DB 2; Length 259;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXASLF 9
|:|:|:|:|
Db 127 GINGWASLF 135

RESULT 14
Q6ZM65 PRELIMINARY; PRT; 263 AA.
AC Q6ZM65;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SI:zK83D9.1 (Novel protein similar to vertebrate aquaporin 3 (AQP3))
DE (Fragment).
GN Name=SI:zK83D9.1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
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RP SEQUENCE FROM N.A.
RA Sehra H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the MIP/aquaporin (TC 1.A.8) family.
DR EMBL; AL844518; CAE50608.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005741; C:mitochondrial outer membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR000425; MIP.
DR Pfam; PF00230; MIP; 1.
DR PRINTS; PR00783; MINTRINSICP.
DR PRODOM; PD000295; MIP; 1.
DR TIGRPS; TIGR00861; MIP; 1.
DR PROSITE; PS00221; MIP; UNKNOWN 1.
KW Porin; Transmembrane; Transport.
FT NON TER 1
SQ SEQUENCE 263 AA; 28190-MW; 51D9D9594F03EA30 CRC64;
Query Match 82.1%; Score 32; DB 2; Length 263;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXASLF 9
|:|:|:|:|
Db 103 GVNATAGIF 111

RESULT 15
CAE50608 PRELIMINARY; PRT; 263 AA.
AC CAE50608;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE SI:zK83D9.1 (Novel protein similar to vertebrate aquaporin 3 (AQP3))
DE (Fragment).
GN SI:zK83D9.1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Sehra H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844518; CAE50608.1; -.
DR PROSITE; PS00221; MIP.
FT NON TER 1
SQ SEQUENCE 263 AA; 28190-MW; 51D9D9594F03EA30 CRC64;
Query Match 82.1%; Score 32; DB 2; Length 263;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXASLF 9
|:|:|:|:|
Db 103 GVNATAGIF 111
```

Search completed: October 26, 2004, 16:05:03
Job time : 42.6324 secs

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GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:15 ; Search time 42.75 Seconds
(without alignments)
75.522 Million cell updates/sec

Title: US-10-032-950-6

Perfect score: 39

Sequence: 1 GVNAXSALF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	94.9	9	3	Aay67856 S. aureus
2	37	94.9	9	5	Aam50904 AgrD-auto
3	37	94.9	9	5	Abp53545 Cyclic pe
4	35	89.7	9	3	Aay67860 Staphyloc
5	35	89.7	9	3	Aay67859 Staphyloc
6	35	89.7	9	5	Abb07160 Peptide-m
7	35	89.7	9	5	Aam50907 Protected
8	35	89.7	9	5	Aam51004 AgrD2 lac
9	35	89.7	9	5	Aam51003 AgrD2 lin
10	35	89.7	9	5	Aam51002 AgrD2 lin
11	34	87.2	9	3	Aay67851 S. aureus
12	34	87.2	9	3	Aay67861 Staphyloc
13	34	87.2	9	5	Abb07161 Peptide-m
14	34	87.2	9	5	Aam51005 AgrD2 lac
15	34	87.2	9	5	Aam50908 Protected
16	34	87.2	9	5	Aam50899 AgrD-auto
17	34	87.2	9	5	Abp53540 Cyclic pe
18	33	84.6	9	2	Aam38323 Transcrip
19	33	84.6	9	5	Abb07159 Peptide-m
20	33	84.6	9	5	Aam51001 AgrD2 thi
21	33	84.6	9	6	Abb4631 S. aureus
22	33	84.6	9	7	Adf09190 S. aureus
23	33	84.6	9	8	Adj98875 Peptide t
24	33	84.6	47	6	Abb84634 S. aureus
25	33	84.6	47	7	Adf09193 S. aureus

26	31	79.5	9	3	Aay67855	S. aureus
27	31	79.5	9	5	Aam50903	AgrD-auto
28	31	79.5	9	5	Abp53544	Cyclic pe
29	30	76.9	9	3	Aay67852	S. aureus
30	30	76.9	9	5	Aam50900	AgrD-auto
31	30	76.9	9	5	Abp53541	Cyclic pe
32	30	76.9	103	4	Abg24179	Novel hum
33	30	76.9	338	6	Abp80927	N. gonorr
34	30	76.9	340	6	Abu25396	Protein e
35	30	76.9	389	3	Aay68973	CpsH pro
36	30	76.9	549	2	Aam98659	H. pylori
37	29	74.4	9	3	Aay67857	S. aureus
38	29	74.4	9	5	Aam50905	AgrD-auto
39	29	74.4	9	5	Abp53546	Cyclic pe
40	29	74.4	96	4	Abg10434	Novel hum
41	29	74.4	255	5	Abb4961	Listeria
42	29	74.4	282	5	Abp26477	Streptoco
43	29	74.4	336	8	Adj48853	Oil-assoc
44	29	74.4	337	7	Adf44608	Wheat fru
45	29	74.4	337	8	Adj48980	Oil-assoc

ALIGNMENTS

RESULT 1

AAy67856

ID AAY67856 standard; peptide; 9 AA.

XX AAY67856;

AC AAY67856;

XX AAY67856;

DT 25-APR-2000 (first entry)

XX S. aureus peptide #6 used for bacterial interference.

DE Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;

XX Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;

KW virulence factor; treatment.

XX Staphylococcus aureus.

OS Staphylococcus aureus.

XX Staphylococcus aureus.

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal residue forms bond with C-terminal

FT residue to form a cyclic peptide"

FT Misc-difference 5

FT /label= Unknown

XX WO9567286-A2.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-US014562.

XX 24-JUN-1998; 98US-00103438.

XX (UYNQ) UNIV ROCKEFELLER.

XX (UYNQ) UNIV NEW YORK STATE.

XX Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX WPI; 2000-147202/13.

XX New cyclic peptides for treating infections with Staphylococcus aureus.

XX Claim 9; Page 26; 37pp; English.

XX This sequence represents a cyclic peptide derived from the Staphylococcus

CC aureus AgrD peptide. The invention relates to AgrD derived peptides, a

CC composition containing a peptide and a carrier, and a method for the

CC production of the cyclic peptides. The peptide inhibits the agr response,

CC which is normally associated with the release of virulence factors of

CC Staphylococcus aureus. An AgrD peptide is produced by S. aureus that

CC activates the agr response in strains of a single group, but interferes

CC with this response in strains of different groups. The peptides and
 CC composition containing them can be used to treat infections by *S. aureus*
 XX
 SQ Sequence 9 AA;

Query Match 94.9%; Score 37; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
 |||||
 DB 1 GVNAXSALF 9

RESULT 2
 ID RAM50904 standard; peptide; 9 AA.
 XX
 AC AAM50904;

DT 08-MAY-2002 (first entry)

DE AgrD-autoinducing cyclic peptide, inhibitor of agr response.

XX Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
 KW antibacterial; infection; therapy; cyclic.
 XX
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"

FT Misc-difference 5 /note= "any amino acid"

FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"

XX US6337385-B1.

XX 08-JAN-2002.

XX 24-JUN-1999; 99US-00339511.

XX 24-JUN-1998; 98US-0090402P.

XX (UYRQ) UNIV ROCKEFELLER.

XX (UTNY) UNIV NEW YORK STATE.

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX WPI; 2002-170774/22.

XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 FT interference and for treating Staphylococcus aureus infection in a
 PT subject.

XX Claim 7; Col 19; 18pp; English.

XX The present sequence is that of a novel synthetic cyclic peptide of the
 CC invention that is capable of inhibiting the agr response of
 CC Staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is
 CC a secreted agr-encoded peptide and where the agr locus controls the
 CC synthesis of virulence factor and other extracellular proteins
 CC responsible for pathogenicity in *S. aureus*. Preferred peptides may have
 CC the sequence NH₂-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z
 CC residue and COOH other than a thioester bond, where X is an amino acid,
 CC an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a
 CC synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The
 CC cyclic bond is especially a lactam or lactone bond. The thiolactone
 CC structure within native AgrD peptides is required for activation of the
 CC agr response. Elimination of the thiol ester component of the cyclic ring
 CC structure can destroy agr response activating activity while preserving
 CC and enhancing inhibitory activity. A claimed method of preparing a cyclic

CC peptide involves: assembling a linear peptide chain on to a solid phase
 CC resin support; deprotecting the resulting protected assembled peptide;
 CC treating the deprotected peptide with neutral buffer for a time
 CC sufficient to form the cyclic peptide and cleave the peptide from the
 CC support; and recovering the cyclic peptide. The peptide is useful for
 CC bacterial interference, especially for the treatment of *S. aureus*
 CC infection

XX Sequence 9 AA;

Query Match 94.9%; Score 37; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
 |||||
 DB 1 GVNAXSALF 9

RESULT 3

ID ABP53545 standard; peptide; 9 AA.

XX ABP53545;

XX 13-DEC-2002 (first entry)

XX Cyclic peptide SEQ ID NO:6.

XX Cyclic peptide; Staphylococcus aureus; infection; antibacterial;
 KW agr response inhibitor.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 5 /note= "any amino acid"

XX US2002077453-A1.

XX 20-JUN-2002.

XX 27-DEC-2001; 2001US-00032950.

XX 24-JUN-1998; 98US-0090402P.

XX 24-JUN-1999; 99US-00339511.

XX (MUIR) MUIR T W.

XX (MAYV) MAYVILLE P.

XX (NOVI) NOVICK R P.

XX (BEAV) BEAVIS R.

XX (JIGG) JI G.

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX WPI; 2002-681366/73.

XX New cyclic peptides, useful for treating Staphylococcus aureus
 PT infections.

XX Claim 9; Page 10; 18pp; English.

XX ABP53540 to ABP53547 represent cyclic peptides (I) from the present
 CC invention. The present invention also describes a method for treating
 CC Staphylococcus aureus infection comprising the administration of a
 CC composition comprising (I). (I) has antibacterial activity and can be
 CC used as an agr gene response inhibitor. The peptides are useful for
 CC treating *S. aureus* infections

XX Sequence 9 AA;

Query Match 94.9%; Score 37; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
 |||||
 DB 1 GVNAXSALF 9

RESULT 4
 AAY67860
 ID AAY67860 standard; peptide; 9 AA.
 AC AAY67860;
 DT 25-APR-2000 (first entry)
 DE Staphylococcus aureus AgrDII derived peptide sequence.
 KW Staphylococcus aureus infection; AgrD; agr response; treatment;
 XW virulence factor.
 XX Staphylococcus aureus.
 OS Staphylococcus aureus.
 PN WO9967286-A2.
 PD 29-DEC-1999.
 PF 24-JUN-1999; 99WO-US014562.
 PR 24-JUN-1998; 98US-00103438.
 XX (UYRQ) UNIV ROCKEFELLER.
 PA (UYNY) UNIV NEW YORK STATE.
 PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;
 DR WPI; 2000-147202/13.
 PT New cyclic peptides for treating infections with Staphylococcus aureus.
 PS Example; Page 22; 37pp; English.
 XX This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus

Sequence 9 AA;
 Query Match 89.7%; Score 35; DB 3; Length 9;
 Best Local Similarity 77.8%; Pred. NO. 1.7e+06;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
 |||||
 DB 1 GVNAXSALF 9

RESULT 6
 ABB07160
 ID ABB07160 standard; peptide; 9 AA.
 AC ABB07160;
 XX 13-MAR-2002 (first entry)
 DT Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
 DE Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
 KW vulnerrary; pheromone; agr system; accessory gene regulator; cyclic.
 XX Synthetic.
 OS WO200185664-A2.
 PN 15-NOV-2001.
 PD 10-MAY-2001; 2001WO-US015221.
 PF 10-MAY-2000; 2000US-0203000P.
 PR 07-DEC-2000; 2000US-0254398P.
 XX (UYPR-) UNIV PRINCETON.
 PA (QUOR-) QUOREX PHARM INC.
 PA (UYTE-) UNIV TECHNOLOGIES INT INC.
 XX Bassler BL, Dammel CS, Schauder S, Shokat K, Stein J, Surette MG;
 PI

XX DR WPI; 2002-075235/10.

XX PT Use of autoinducer-2 agonists or antagonists for regulating activity of

XX PT autoinducer-2 receptor, regulating bacterial growth and pathogenesis,

XX PT also antibiotic compositions.

XX PS Disclosure; Page 33; 134pp; English.

XX CC The invention relates to the use of autoinducer-2 (AI-2) agonists or

XX CC antagonists for regulating activity of autoinducer-2 receptor, regulating

XX CC bacterial growth and pathogenesis. Synergistic antibiotic compositions

XX CC comprising inhibitors of the quorum-sensing pathway of a microorganism

XX CC are also provided. Methods using such AI-2 analogues are useful for

XX CC treating pathogen-associated disease states. The compounds and antibiotic

XX CC compositions can be used to inhibit bacterial cell growth and/or biofilm

XX CC formation on a medical device, particularly for promoting growth of skin

XX CC graft replacements used in the treatment of burns and ulcers. They may

XX CC also be used to aid wound repair, and to inhibit bacterial cell growth

XX CC and biofilm formation in or on products or devices used for personal

XX CC hygiene. The present sequence represents a inhibitor of peptide-mediated

XX CC quorum sensing

XX SQ Sequence 9 AA;

Query Match 89.7%; Score 35; DB 5; Length 9;

Best Local Similarity 77.8%; Pred. No. 1.7e+06;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSALF 9
|||||:|

Db 1 GVNASSSLF 9

RESULT 7

AA050907

ID AAM50907 standard; peptide; 9 AA.

XX AC AAM50907;

XX DT 08-MAY-2002 (first entry)

XX DE Protected peptide used in cyclic peptide production.

XX KW Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;

XX KW antibacterial; infection; therapy; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Z-Gly"

FT Misc-difference 5

FT /note= "note linked to residue 9 to form cyclic peptide"

FT Modified-site 5

FT /note= "Ser(tBu)"

FT Modified-site 6

FT /note= "Ser(Bzl)"

FT Modified-site 7

FT /note= "Ser(Bzl)"

FT Misc-difference 9

FT /note= "note linked to residue 5 to form cyclic peptide"

XX US6337385-B1.

PN 08-JAN-2002.

XX 24-JUN-1999; 99US-00339511.

XX 24-JUN-1998; 98US-0090402P.

XX (UYRQ) UNIV ROCKEFELLER.

XX (UYNY) UNIV NEW YORK STATE.

XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX XI WPI; 2002-170774/22.

XX DR Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial

XX PT interference and for treating Staphylococcus aureus infection in a

XX PT subject.

XX PS Disclosure; Col 14; 18pp; English.

XX CC The present sequence is that of a protected peptide used in an example of

XX CC the preparation of novel synthetic cyclic peptides of the invention (see

XX CC AAM50899-906). The peptide corresponds to the Staphylococcus aureus

XX CC AgrDII sequence with a Cys45 to Ser mutation (lactone). It was synthesised

XX CC on a Wang-resin using an Fmoc N-alpha protection strategy. Following

XX CC chain assembly, the peptide was cleaved from the support and the Ser-5

XX CC residue deprotected by treatment with a trifluoroacetic

XX CC acid:anisole:water mixture (90:5:5) for 4 hr. The partially protected

XX CC peptide-alpha carboxylates were then dissolved in DMF and treated with

XX CC PyBOP and a catalytic amount of dimethylaminopyridine. Cyclization was

XX CC complete after 2 hr. The remaining protecting groups were then removed by

XX CC treatment with HF and the peptide purified by HPLC. The cyclic peptide is

XX CC capable of inhibiting the agr response of Staphylococcus aureus. The

XX CC thiolactone structure within native AgrD peptides is required for

XX CC activation of this response. Replacement of the thiol ester component of

XX CC the cyclic ring structure with a lactone (as in the present case) or a

XX CC lactam can destroy agr response activating activity while preserving and

XX CC enhancing inhibitory activity. The cyclic peptides are useful for

XX CC bacterial interference, especially for the treatment of S. aureus

XX CC infection

XX SQ Sequence 9 AA;

Query Match 89.7%; Score 35; DB 5; Length 9;

Best Local Similarity 77.8%; Pred. No. 1.7e+06;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSALF 9
|||||:|

Db 1 GVNASSSLF 9

RESULT 8

AA051004

ID AAM51004 standard; peptide; 9 AA.

XX AC AAM51004;

XX DT 07-AUG-2003 (revised)

XX DT 08-MAY-2002 (first entry)

XX DE AgrD2 lactone cyclic peptide.

XX KW AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;

XX KW therapy; lactone; cyclic.

XX OS Staphylococcus aureus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 5

FT /note= "note linked to residue 9 to form cyclic peptide"

FT Misc-difference 9

FT /note= "note linked to residue 5 to form cyclic peptide"

XX US6337385-B1.

PN 08-JAN-2002.

XX 24-JUN-1999; 99US-00339511.

XX 24-JUN-1998; 98US-0090402P.

```

XX PA (UYRQ ) UNIV ROCKEFELLER.
XX PA (UYNV ) UNIV NEW YORK STATE.
XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX DR WPI; 2002-170774/22.
XX XX
XX PT Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
XX PT interference and for treating Staphylococcus aureus infection in a
XX PT subject.
XX PS Example 1; Col 9; 18pp; English.
XX CC The present sequence is that of a novel synthetic AgrD2 linear free acid
XX CC peptide in which residue 5 of the peptide is linked to residue 9 via a
XX CC lactone bond. The peptide is derived from an AgrD2 peptide of
XX CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
XX CC where the agr locus controls the synthesis of virulence factor and other
XX CC extracellular proteins responsible for pathogenicity in S. aureus. The
XX CC biological activity of the synthetic peptide was assayed using cultured
XX CC S. aureus strains containing a beta-lactamase reporter gene fused to the
XX CC agrP3 promoter. This allowed activation or inhibition of the agr response
XX CC to be monitored spectrophotometrically. The lactone AgrD2 peptide
XX CC inhibited the agr response of group I S. aureus strains without
XX CC activating the agr response in group I, II or III strains. The invention
XX CC provides claimed cyclic peptides (see AAM50899-906 and AAM50999) and
XX CC methods for preparing them, especially peptides where the cyclic bond is
XX CC a lactam or lactone bond. The cyclic peptides are useful for bacterial
XX CC interference, especially for the treatment of S. aureus infection.
XX CC (Updated on 07-AUG-2003 to correct OS field.)
XX SQ Sequence 9 AA;
XX
XX Query Match 89.7%; Score 35; DB 5; Length 9;
XX Best Local Similarity 77.8%; Pred. NO. 1.7e+06;
XX Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 GVNAXSALF 9
XX Db |||||:|
XX 1 GVNASSSLF 9
XX
XX RESULT 10
XX AAM51002
XX ID AAM51002 standard; peptide; 9 AA.
XX AC AAM51002;
XX XX
XX DT 08-MAY-2002 (first entry)
XX DE AgrD2 linear thioester peptide.
XX XX
XX KW AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
XX therapy.
XX OS Staphylococcus aureus.
XX XX
XX FH Key Location/Qualifiers
XX FT Modified-site 9 /note= "C-terminal thioester"
XX FT
XX PN US6337385-B1.
XX XX
XX PD 08-JAN-2002.
XX XX
XX PF 24-JUN-1999; 99US-00339511.
XX XX
XX PR 24-JUN-1998; 98US-0090402P.
XX XX
XX PA (UYRQ ) UNIV ROCKEFELLER.
XX PA (UYNV ) UNIV NEW YORK STATE.
XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX DR WPI; 2002-170774/22.
XX XX
XX PT Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
XX PT interference and for treating Staphylococcus aureus infection in a
XX PT subject.
XX XX

```

PS Example 1; Col 9; 18pp; English.

XX The present sequence is that of a novel synthetic AgrD2 linear thioester
CC peptide. The peptide is derived from the cyclic AgrD2 peptide of
CC *Staphylococcus aureus* group II. AgrD2 is a secreted agr-encoded peptide,
CC where the agr locus controls the synthesis of virulence factor and other
CC extracellular proteins responsible for pathogenicity in *S. aureus*. The
CC biological activity of the synthetic peptide was assayed using cultured
CC *S. aureus* strains containing a beta-lactamase reporter gene fused to the
CC agrP3 promoter. This allowed activation or inhibition of the agr response
CC to be monitored spectrophotometrically. Unlike an AgrD2 thiolactone
CC cyclic peptide (see AM51001), the present peptide was unable to either
CC activate or inhibit the agr response, even when added to cultured cells
CC at uM concentrations. The invention provides claimed cyclic peptides (see
CC AM50899-906 and AM50999) and methods for preparing them. The cyclic
CC peptides are useful for bacterial interference, especially for the
CC treatment of *S. aureus* infection

XX Sequence 9 AA;

Query Match 89.7%; Score 35; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSALF 9
Db 1 GVNAXSSLF 9

RESULT 11

ID AAY67851 standard; peptide; 9 AA.

XX AAY67851;

XX 25-APR-2000 (first entry)

XX *S. aureus* peptide #1 used for bacterial interference.

XX *Staphylococcus aureus* infection; cyclic peptide; AgrD; agr response;
XX virulence factor; treatment.

XX *Staphylococcus aureus*.

XX Key Location/Qualifiers
FH Misc-difference 5
FT /label= Unknown

XX WO9967286-A2.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-US014562.

XX 24-JUN-1998; 98US-00103438.

XX (UYRO) UNIV ROCKEFELLER.

XX (UNY) UNIV NEW YORK STATE.

XX Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX WPI; 2000-147202/13.

XX New cyclic peptides for treating infections with *Staphylococcus aureus*.

XX Claim 9; Page 26; 37pp; English.

XX This sequence represents a cyclic peptide derived from the *Staphylococcus*
CC *aureus* AgrD peptide. The invention relates to AgrD derived peptides, a
CC composition containing a peptide and a carrier, and a method for the
CC production of the cyclic peptides. The peptide inhibits the agr response,
CC which is normally associated with the release of virulence factors of
CC *Staphylococcus aureus*. An AgrD peptide is produced by *S. aureus* that

CC activates the agr response in strains of a single group, but interferes
CC with this response in strains of different groups. The peptides and
CC composition containing them can be used to treat infections by *S. aureus*
XX Sequence 9 AA;

Query Match 87.2%; Score 34; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVNAXSALF 9
Db 1 GVNAXSSLF 9

RESULT 12

ID AAY67861 standard; peptide; 9 AA.

XX AAY67861;

XX 25-APR-2000 (first entry)

XX *Staphylococcus aureus* AgrDII derived peptide sequence.

XX *Staphylococcus aureus* infection; AgrD; agr response; treatment;
XX virulence factor.

XX *Staphylococcus aureus*.

XX Key Location/Qualifiers
FH Misc-difference 5
FT /label= Unknown

XX WO9967286-A2.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-US014562.

XX 24-JUN-1998; 98US-00103438.

XX (UYRO) UNIV ROCKEFELLER.

XX (UNY) UNIV NEW YORK STATE.

XX Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX WPI; 2000-147202/13.

XX New cyclic peptides for treating infections with *Staphylococcus aureus*.

XX Example; Page 22; 37pp; English.

XX This sequence represents the *Staphylococcus aureus* AgrDII derived
CC peptide. The invention relates to AgrD derived cyclic peptides, a
CC composition containing a peptide and a carrier, and a method for the
CC production of the cyclic peptides. The peptide inhibits the agr response,
CC which is normally associated with the release of virulence factors of
CC *Staphylococcus aureus*. An AgrD peptide is produced by *S. aureus* that
CC activates the agr response in strains of a single group, but interferes
CC with this response in strains of different groups. The peptides and
CC composition containing them can be used to treat infections by *S. aureus*

XX Sequence 9 AA;

Query Match 87.2%; Score 34; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVNAXSALF 9
Db 1 GVNAXSSLF 9

XX	AAW50908;
XX	08-MAY-2002 (first entry)
XX	Protected peptide used in cyclic peptide production.
XX	Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
XX	antibacterial; infection; therapy; cyclic.
XX	Synthetic.
OS	
XX	Key
XX	Location/Qualifiers
PH	Modified-site 1 /note= "2-Gly"
FT	
FT	Misc-difference 5
FT	/note= "note linked to residue 9 to form cyclic peptide"
FT	
FT	Modified-site 5
FT	/label= Dpr(Boc)
FT	
FT	Modified-site 6
FT	/note= "Ser(Bzl)"
FT	
FT	Modified-site 7
FT	/note= "Ser(Bzl)"
FT	
FT	Misc-difference 9
FT	/note= "note linked to residue 5 to form cyclic peptide"
FT	
XX	US637385-B1.
PN	
XX	08-JAN-2002.
PD	
XX	24-JUN-1999; 99US-00339511.
XX	
XX	24-JUN-1998; 98US-0090402P.
XX	
XX	(UFRQ) UNIV ROCKEFELLER.
PA	(UNY) UNIV NEW YORK STATE.
XX	
XX	Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX	WPI; 2002-170774/22.
XX	
XX	Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
PT	interference and for treating Staphylococcus aureus infection in a
PT	subject.
XX	
PS	Disclosure; Col 14; 18pp; English.
XX	
XX	The present sequence is that of a protected peptide used in an example of
CC	the preparation of novel synthetic cyclic peptides of the invention (see
CC	AAW50899-908). The peptide corresponds to the Staphylococcus aureus
CC	AgrDII sequence with a Cys5 to diaminopropionic acid (Dpr) mutation
CC	(lactam). It was synthesised on a Wang-resin using an Fmoc N-alpha
CC	protection strategy. Following chain assembly, the peptide was cleaved
CC	from the support and the Dpr-5 residue deprotected by treatment with a
CC	trifluoroacetic acid:anisole:water mixture (90:5:5) for 4 hr. The
CC	partially protected peptide-alpha carboxylates were then dissolved in DMF
CC	and treated with PyBOP. Cyclization was complete after 2 hr. The
CC	remaining protecting groups were removed by treatment with HF and the
CC	peptide purified by HPLC. The cyclic peptide is capable of inhibiting the
CC	agr response of Staphylococcus aureus. The thiolactone structure with
CC	native AgrD peptides is required for activation of this response.
CC	Replacement of the thiol ester component of the cyclic ring structure
CC	with a lactam (as in the present case) or a lactone can destroy agr
CC	response activating activity while preserving and enhancing inhibitory
CC	activity. The cyclic peptides are useful for bacterial interference,
CC	especially for the treatment of S. aureus infection
XX	
SQ	Sequence.9 AA;

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Qy      1  GVNXSALF  9
        |||||:|
Db      1  GVNXSSUF  9

Search completed: October 26, 2004, 15:59:45
Job time : 43.75 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:54:00 ; Search time 31.5 Seconds
(without alignments)
92.502 Million cell updates/sec

Title: US-10-032-950-6

Perfect score: 39

Sequence: 1 GVNAXSALF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	37	94.9	9	13	US-10-032-950-6
2	34	87.2	9	13	Sequence 6, Appli
3	33	84.6	9	14	US-10-032-950-1
4	33	84.6	47	14	Sequence 1, Appli
5	31	79.5	9	13	US-10-201-444-3
6	30	76.9	9	13	Sequence 6, Appli
7	30	76.9	340	15	US-10-032-950-5
8	30	76.9	388	9	US-10-032-950-2
9	30	76.9	508	14	US-10-282-122A-53320
10	30	76.9	549	10	Sequence 33, Appli
11	29	74.4	9	13	US-09-767-041-33
12	29	74.4	139	16	US-10-369-493-19084
13	29	74.4	187	16	Sequence 184, App
					Sequence 7, Appli
					Sequence 113791,
					Sequence 144131,

14	29	74.4	266	16	US-10-767-701-40852	Sequence 40852, A
15	29	74.4	336	15	US-10-389-566-857	Sequence 857, App
16	29	74.4	337	14	US-10-004-502-12	Sequence 12, Appl
17	29	74.4	337	15	US-10-389-566-984	Sequence 984, App
18	29	74.4	370	15	US-10-425-114-60718	Sequence 60718, A
19	29	74.4	391	14	US-10-156-761-9222	Sequence 9222, Ap
20	29	74.4	442	15	US-10-282-122A-53013	Sequence 53013, A
21	29	74.4	468	14	US-10-369-493-12194	Sequence 12194, A
22	29	74.4	605	9	US-09-841-132-574	Sequence 574, App
23	28	71.8	9	13	US-10-032-950-4	Sequence 4, Appli
24	28	71.8	60	15	US-10-424-599-260806	Sequence 260806, A
25	28	71.8	71	16	US-10-767-701-59048	Sequence 59048, A
26	28	71.8	101	15	US-10-424-599-143938	Sequence 143938, A
27	28	71.8	127	16	US-10-437-963-137791	Sequence 137791, A
28	28	71.8	122	11	US-09-864-408A-7538	Sequence 7538, Ap
29	28	71.8	131	16	US-10-767-701-52970	Sequence 52970, A
30	28	71.8	139	16	US-10-767-701-61617	Sequence 61617, A
31	28	71.8	144	9	US-09-894-018-129	Sequence 129, App
32	28	71.8	255	14	US-10-083-357-1280	Sequence 1280, Ap
33	28	71.8	273	15	US-10-425-114-64933	Sequence 64933, A
34	28	71.8	284	15	US-10-282-122A-45650	Sequence 45650, A
35	28	71.8	313	16	US-10-437-963-189388	Sequence 189388, A
36	28	71.8	322	10	US-09-866-050A-141	Sequence 141, App
37	28	71.8	332	15	US-10-284-237-2080	Sequence 2080, Ap
38	28	71.8	335	15	US-10-282-122A-47541	Sequence 47541, A
39	28	71.8	338	9	US-09-815-242-5727	Sequence 5727, Ap
40	28	71.8	341	9	US-09-820-044-2	Sequence 2, Appli
41	28	71.8	341	15	US-09-815-242-12158	Sequence 12158, A
42	28	71.8	341	15	US-10-282-122A-44158	Sequence 44158, A
43	28	71.8	354	15	US-10-282-122A-72396	Sequence 72396, A
44	28	71.8	431	10	US-09-866-050A-341	Sequence 341, App
45	28	71.8	431	14	US-10-004-378A-129	Sequence 129, App

ALIGNMENTS

RESULT 1

US-10-032-950-6
; Sequence 6, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-6

Query Match 94.9%; Score 37; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9

Db 1 GVNAXSALF 9
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US-10-032-950-1
; Sequence 1, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-23IN
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-1
Query Match 87.2%; Score 34; DB 13; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVNAXSALF 9
|||||||
Db 1 GVNAXSALF 9
RESULT 3
US-10-201-444-3
; Sequence 3, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT APPLICATION NUMBER: US/10/201,444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-3
Query Match 84.6%; Score 33; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

US-10-201-444-6
; Sequence 6, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT APPLICATION NUMBER: US/10/201,444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-6
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Best Local Similarity 77.8%; Pred. No. 3.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GVNAXSALF 9
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Db 24 GVNACSSLF 32
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US-10-032-950-5
; Sequence 5, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-23IN
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-5
Query Match 79.5%; Score 31; DB 13; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVNAXSALF 9
|||||||
Db 1 GVNAXSALF 9
RESULT 5
US-10-032-950-2
; Sequence 2, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-23IN
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-2
Query Match 79.5%; Score 31; DB 13; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVNAXSALF 9
|||||||
Db 1 GVNAXSALF 9
RESULT 6
US-10-032-950-2
; Sequence 2, Application US/10032950
; Publication No. US20020077453A1


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; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US2002007453Alick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-2
Query Match 76.9%; Score 30; DB 13; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNXASLAF 9
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DB 1 GANAXSSLF 9

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; Sequence 53320, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
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; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53320
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-53320
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Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNXASLAF 9
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DB 98 GINSGAALF 106

RESULT 8
US-09-767-041-33
; Sequence 33, Application US/09767041
; Patent No. US20020055168A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Hilda
; TITLE OF INVENTION: STREPTOCOCCUS SUIIS VACCINES AND DIAGNOSTIC TESTS
; FILE REFERENCE: 2183-4726
; CURRENT APPLICATION NUMBER: US/09/767,041
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/NL93/00460
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: EP98202465.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: EP98202467.1
; PRIOR FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Streptococcus suis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: CPS1H
US-09-767-041-33
Query Match 76.9%; Score 30; DB 9; Length 388;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNXASLAF 9
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DB 335 GYNGETALF 343

RESULT 9
US-10-369-493-19084
; Sequence 19084, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
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; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13084
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Anabaena PCC7120
US-10-369-493-19084

Query Match 76.9%; Score 30; DB 14; Length 508;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSAL 8
: : : : :
Db 156 GINAISAL 163

RESULT 10

US-09-882-227-184
; Sequence 184, Application US/09882227
; Publication No. US20030158396A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20030158396A1 Helicobacter Polypeptides in the
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/047002
; CURRENT APPLICATION NUMBER: US/09/882,227
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/902,615
; PRIOR FILING DATE: 1997-07-29
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-882-227-184

Query Match 76.9%; Score 30; DB 10; Length 549;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
: : : : :
Db 406 GINALSVIF 414

RESULT 11

US-10-032-950-7
; Sequence 7, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, GuangYong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-7

Query Match 74.4%; Score 29; DB 13; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
: : : : :
Db 1 GVNAXSSAF 9

RESULT 12

US-10-437-963-113791
; Sequence 113791, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 113791
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17545C.1.pep
US-10-437-963-113791

Query Match 74.4%; Score 29; DB 16; Length 139;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
: : : : :
Db 41 GIRAASALF 49

RESULT 13

US-10-437-963-144131
; Sequence 144131, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963

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; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 144131
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44976C.1.pep
US-10-437-963-144131

Query Match          74.4%; Score 29; DB 16; Length 187;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 VNAXSALF 9
      ||| |||
Db      140 VNASSAVF 147

RESULT 14
US-10-767-701-40852
; Sequence 40852, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kowalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 40852
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C105350_1.pep
US-10-767-701-40852

Query Match          74.4%; Score 29; DB 16; Length 266;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GVNAXSALF 9
      ||| |||
Db      193 GVEAAALF 201

RESULT 15
US-10-389-566-857
; Sequence 857, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 857
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Triticum aestivum
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US-10-389-566-857

Query Match          74.4%; Score 29; DB 15; Length 336;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GVNAXSALF 9
      ||| |||
Db      89 GVNAGCLF 97

Search completed: October 26, 2004, 16:10:13
Job time : 32.5 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:46:55 ; Search time 8.73529 Seconds
(without alignments)
99.132 Million cell updates/sec

Title: US-10-032-950-6

Perfect score: 39

Sequence: 1 GVNAXSALF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	84.6	47	2 C89995	AgRD protein [limpo
2	32	82.1	382	2 A28067	lysosomal membrane
3	32	82.1	405	2 A60534	P2B/LAMP-1 precurs
4	32	82.1	407	2 A30200	120K lysosomal mem
5	31	79.5	333	1 C69812	ferrichrome ABC tr
6	31	79.5	442	2 A23339	manganese transpor
7	31	79.5	1049	2 T30325	alpha-mannosidase
8	30	76.9	234	2 S60885	ferric exochelin u
9	30	76.9	298	2 T22250	lysosomal membrane
10	30	76.9	361	2 AD3198	hypothetical prote
11	30	76.9	533	2 AG2328	2,3-bisphosphoglyc
12	30	76.9	549	2 P64640	conserved phosphat
13	29	74.4	188	2 G84041	hypothetical prote
14	29	74.4	250	2 AD0421	flnnp protein [limpo
15	29	74.4	255	2 AB1159	flagellar biosynth
16	29	74.4	255	2 AD1518	flagellar biosynth
17	29	74.4	269	2 S58439	transcription fact
18	29	74.4	346	2 S55491	probable galactosyl
19	29	74.4	605	2 H71562	probable flagellin
20	29	74.4	895	2 T45786	receptor-protein x
21	29	74.4	1016	2 T30943	aminopeptidase (EC
22	29	74.4	1016	2 T30942	aminopeptidase (EC
23	29	74.4	1421	2 T34225	hypothetical prote
24	28	71.8	43	2 S20039	hypothetical prote
25	28	71.8	43	2 S20040	hypothetical prote
26	28	71.8	148	2 D97308	probable membrane
27	28	71.8	167	2 G87610	hypothetical prote
28	28	71.8	259	2 H75481	hydrolase, CbX/Cb
29	28	71.8	303	2 D84230	hypothetical prote

30 28 71.8 341 2 G89996 hypothetical prote
31 28 71.8 346 2 F69786 glycoprotein endop
32 28 71.8 389 1 S36633 xpsd protein - sec
33 28 71.8 394 2 E81286 probable polysacch
34 28 71.8 452 2 F64053 4-chlorobenzoate-C
35 28 71.8 488 1 WMBE42 DNA-binding protei
36 28 71.8 491 2 D95366 NADH2 dehydrogenas
37 28 71.8 546 2 A32260 cholesterol oxidas
38 28 71.8 573 2 P81313 peptidase (W3 fami
39 28 71.8 631 2 D89750 phosphotransferase
40 28 71.8 655 2 G89189 protein Y32F6A.3 (
41 28 71.8 803 2 T39530 hypothetical prote
42 28 71.8 832 2 S46706 probable transcrip
43 28 71.8 870 2 S74291 hypothetical prote
44 28 71.8 926 2 S48463 SEC24 protein - ve
45 28 71.8 1844 1 RRPPTM genome polypeptin

ALIGNMENTS

RESULT 1

C89995 AgRD protein [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: C89995

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiranatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.

A:Reference number: A89758; UID:21311952; PMID:11418146

A:Accession: C89995

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-47 <KUR>

A:Cross-references: UNIPROT:O33586; GB:BA000018; PID:gl3701831; PIDN:BA843124.1; GSPDB:

A:Experimental source: strain N315

C:Genetics:

A:Gene: agrD

Query Match 84.6%; Score 33; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 0.81; Mismatches 1; Indels 1; Gaps 0;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;
QY 1 GVNAXSALF 9
Db 24 GVNACSSLF 32

RESULT 2

A28067 lysosomal membrane glycoprotein LAMP-1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C:Accession: A28067

R:Chen, J.W.; Chn, Y.; Yuxsel, K.U.; Gracy, R.W.; August, J.T.

J. Biol. Chem. 263, 8754-8759, 1988

A:Title: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprot

A:Reference number: A28067; UID:88243732; PMID:3379044

A:Accession: A28067

A:Molecule type: mRNA

A:Residues: 1-382 <CHE>

A:Cross-references: UNIPROT:P11438; GB:J03881; NID:G198706; PIDN:AAA39411.1; PID:929369;

A>Note: the authors translated the codon ATT for residue 1 as Leu and CCG for residue 2

C:Superfamily: lysosome-associated membrane protein

C:Keywords: glycoprotein; membrane protein

Query Match 82.1%; Score 32; DB 2; Length 382;

Best Local Similarity 66.7%; Pred. No. 12; Mismatches 2; Indels 1; Gaps 0;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 0;

C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30525
R;Rades, C.J.; Gilbert, A.; Goodman, C.D.; Hintz, W.E.
Glycobiology 8, 17-33, 1998
A;Title: Identification and analysis of a class 2 alpha-mannosidase in Aspergillus nidulans
A;Reference number: Z20843; MUID:98119762; PMID:9451011
A;Accession: T30525
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1049 <EAD>
A;Cross-references: UNIPROT:O13344; EMBL:AF016850; NID:q2407175; PID:q2407176; PIDN:AAB7
C;Genetics:
A;Introns: 49/2; 213/1; 877/2
A;Note: med2
C;Superfamily: Saccharomycetes alpha-mannosidase
C;Keywords: glycosidase; hydrolase

Query Match 79.5%; Score 31; DB 2; Length 1049;
Best Local Similarity 87.5%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VNAXSALF 9
||| :|||
Db 979 VNAXSALF 986

RESULT 8
S60885
feric exochelin uptake protein fxuC - Mycobacterium smegmatis (fragment)
C;Species: Mycobacterium smegmatis
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S60885
R;Fiss, E.H.; Yu, S.; Jacobs Jr., W.R.
Mol. Microbiol. 14, 557-569, 1994
A;Title: Identification of genes involved in the sequestration of iron in mycobacteria:
A;Reference number: S60885; MUID:95191405; PMID:7885234
A;Accession: S60885
A;Molecule type: DNA
A;Residues: 1-234 <FIS>
A;Cross-references: UNIPROT:Q50375; EMBL:U10425; NID:g595400; PIDN:AAC43258.1; PID:g5954
C;Genetics:
A;Gene: fxuC

Query Match 76.9%; Score 30; DB 2; Length 234;
Best Local Similarity 55.6%; Pred. No. 22;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
||| :|||
Db 37 GINSALF 45

RESULT 9
T22250
hypothetical protein F45H11.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22250
R;Kelly, P.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19537
A;Accession: T22250
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-298 <WIL>
A;Cross-references: UNIPROT:Q93727; EMBL:Z78420; PIDN:CAB01709.1; GSPDB:GNC00019; CBSP:F4
A;Experimental source: clone F45H11
C;Genetics:
A;Gene: CBSP:F45H11.1
A;Map position: 1
A;Introns: 52/3; 109/2; 177/3; 248/1; 290/3

Query Match 76.9%; Score 30; DB 2; Length 238;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSAL 8
||| :|||
Db 159 GINAQSAL 166

RESULT 10
AD3198
hypothetical protein fepD [imported] - Agrobacterium tumefaciens (strain C58, Dupont) p
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AD3198
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3198
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-361 <KUR>
A;Cross-references: UNIPROT:Q8UK10; GB:AE008687; PIDN:AAL46002.1; PID:gl7743757; GSPDB:
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: fepD
A;Genome: plasmid

Query Match 76.9%; Score 30; DB 2; Length 361;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
||| :|||
Db 122 GVNAGAAFF 130

RESULT 11
AG2328
2,3-bisphosphoglycerate-independent phosphoglycerate mutase [imported] - Nostoc sp. (st
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG2328
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2328
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-533 <KUR>
A;Cross-references: UNIPROT:Q8YPL2; GB:BA000019; PIDN:BA075881.1; PID:gl7133317; GSPDB:
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4182
C;Superfamily: cofactor-independent phosphoglycerate mutase

Query Match 76.9%; Score 30; DB 2; Length 533;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSAL 8
||| :|||
Db 163 GINAISAL 170

RESULT 12

F64640
 conserved hypothetical protein HP0966 - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C:Accession: F64640
 R:Tomb, J.F.; White, O.; Karlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Knaplak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: F64640
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-549 <TOM>
 A:Cross-references: UNIPROT:O25619; GB:AE000605; GB:AE000511; NID:g2314103; PIDN:AAD0801

Query Match 76.9%; Score 30; DB 2; Length 549;
 Best Local Similarity 55.6%; Pred. No. 53;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GVNAXSALF 9
 Db 406 GINALSVIF 414

RESULT 13

G84041
 hypothetical protein BH3135 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: G84041
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: G84041
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-188 <STO>
 A:Cross-references: UNIPROT:Q9K971; GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA8069
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3135

Query Match 74.4%; Score 29; DB 2; Length 188;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
 Db 60 GLTATSALF 68

RESULT 14

AB0421
 PNP protein [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AB0421
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
 A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AB0421
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-250 <KUR>
 A:Cross-references: UNIPROT:Q82BF1; GB:AL590842; PIDN:CAC92694.1; PID:GI5981389; GSPDB:G

C:Genetics:

A:Gene: phnP
 C:Superfamily: ATP-binding protein PhnP (PhnP)

Query Match 74.4%; Score 29; DB 2; Length 250;
 Best Local Similarity 66.7%; Pred. No. 40;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
 Db 165 GLSADSALF 173

RESULT 15

AD1159
 flagellar biosynthetic protein FlpP homolog lmo0676 [imported] - Listeria monocytogenes
 C:Species: Listeria monocytogenes
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AD1159
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
 A:Authors: Krest, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, O.K.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AD1159
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-255 <GLA>
 A:Cross-references: UNIPROT:Q8Y958; GB:NC_003210; PIDN:CAC98754.1; PID:GI6410065; GSPDB:G
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo0676
 C:Superfamily: flagellar biosynthetic protein flpP

Query Match 74.4%; Score 29; DB 2; Length 255;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
 Db 47 GVNSSVALF 55

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:50 ; Search time 40.6324 Seconds
(without alignments)
127.445 Million cell updates/sec

Title: US-10-032-950-6

Perfect score: 39

Sequence: 1 GVNAXGALF 9

Scoring table: BLCSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	84.6	47	2 Q3586	Q3586 staphylococ
2	33	84.6	47	2 Q7A2N4	Q7A2N4 staphylococ
3	33	84.6	47	2 Q7A417	Q7A417 staphylococ
4	33	84.6	47	2 CAE92745	Ca92745 staphyloc
5	33	84.6	47	2 CAE92748	Ca92748 staphyloc
6	33	84.6	47	2 CAE92751	Ca92751 staphyloc
7	33	84.6	47	2 CAE92754	Ca92754 staphyloc
8	33	84.6	47	2 CAE92757	Ca92757 staphyloc
9	32	82.1	46	2 Q9FLU5	Q9FLU5 staphylococ
10	32	82.1	189	2 Q922T9	Q922T9 mus muscucu
11	32	82.1	406	1 LMP1_MOUSE	P11438 mus muscucu
12	32	82.1	406	2 Q8VH34	Q8VH34 mus muscucu
13	32	82.1	407	1 LMP1_RAT	P14562 rattus norv
14	32	82.1	407	2 Q9DCI3	Q9DCI3 mus muscucu
15	32	82.1	452	2 Q7P724	Q7P724 fusobacteri
16	32	82.1	452	2 Q8RGL3	Q8RGL3 fusobacteri
17	32	82.1	917	2 Q6FM76	Q6FM76 candida gla
18	31	79.5	308	1 GPDA_SYNEL	Q8dh49 synecococc
19	31	79.5	333	2 Q34933	Q34933 bacillus su
20	31	79.5	442	1 MNTH_ANASP	Q8zsb0 anabaena sp
21	31	79.5	493	2 Q72N02	Q72N02 leptospira
22	31	79.5	493	2 Q8F8N1	Q8F8N1 leptospira
23	31	79.5	493	2 AAS71586	Aas71586 leptospir
24	31	79.5	578	2 Q9PKY0	Q9PKY0 chlamydia m
25	31	79.5	1049	2 Q13344	Q13344 emericella
26	30	76.9	234	2 Q50375	Q50375 mycobacteri
27	30	76.9	298	2 Q93727	Q93727 caenorhabdi
28	30	76.9	337	2 Q8XW78	Q8XW78 clostridium
29	30	76.9	344	2 Q8ETK0	Q8ETK0 oenobacil
30	30	76.9	361	2 Q7D3D6	Q7D3D6 agrobacteri
31	30	76.9	361	2 Q8UK10	Q8UK10 agrobacteri

32 30 76.9 388 2 Q9RG47 streptococc
33 30 76.9 533 1 GPML_ANASP
34 30 76.9 549 2 Q25619
35 30 76.9 697 2 Q6FAA6 helicobacte
36 30 76.9 1225 2 Q6GN12 acinetobact
37 30 76.9 1795 2 Q93UY8 xenopus lae
38 29 74.4 56 2 Q70LO6 agrobacteri
39 29 74.4 56 2 CAD92465 convolvul
40 29 74.4 188 2 Q9K871 bacillus ha
41 29 74.4 196 2 Q9CLC1 pasteurella
42 29 74.4 224 2 Q6C345 yarrowia li
43 29 74.4 250 2 Q8ZBF1 yersinia pe
44 29 74.4 250 2 AAS60887 yersinia
45 29 74.4 255 2 Q92DX7 listeria in

ALIGNMENTS

RESULT 1

Q3586 PRELIMINARY; PRT; 47 AA.
AC Q3586;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE AgrD.
GN Name=agrD;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus;
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SA502A;
RX MEDLINE=97342847; PubMed=9197262;
RA Ji G., Beavis R., Novick R.P.;
RT "Bacterial interference caused by autoinducing peptide variants.";
RL Science 276:2027-2030(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Gt31a-cp5, Gt31b-cp5, Gt36a-cp8, Gt36b-cp8, and Gt111-cp8;
RA Goerke C., Dasbach S., Kummel M., Wolz C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001782; AAB63265.1; -
DR EMBL; AJ617715; CAE92745.1; -
DR EMBL; AJ617716; CAE92748.1; -
DR EMBL; AJ617717; CAE92751.1; -
DR EMBL; AJ617718; CAE92754.1; -
DR EMBL; AJ617719; CAE92757.1; -
DR PIR; C89995; C89995.
DR InterPro; IPR009229; AgrD.
DR Pfam; PF05931; AgrD; 1.
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 84.6%; Score 33; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 5.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXGALF 9

|||||
Db 24 GVNACSLF 32

RESULT 2

Q7A2N4 PRELIMINARY; PRT; 47 AA.
ID Q7A2N4;
AC Q7A2N4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE AgrD protein.
GN Name=agrD; OrderedLocusNames=SAV2037;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).

OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=158878; [1]
RN	SEQUENCE FROM N.A.
RP	SEQUENCE 21311952; PubMed=11418146;
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA	Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA	Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus
RT	"aureus.";
RL	Lancet 357;1225-1240(2001).
DR	EMBL; AF003364; BAB3119.1; -
DR	InterPro; IPR009229; AgrD.
DR	Pfam; PF05931; AgrD; 1.
KW	Complete proteome.
QY	SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
DB	24 GVNAXSLF 32
RESULT 3	
Q7A417	PRELIMINARY; PRT; 47 AA.
ID	Q7A417
AC	Q7A417
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	AgrD protein.
GN	Name=agrD; OrderedLocusNames=SA1842.1; ORFNames=SA5066;
OS	Staphylococcus aureus (strain N315).
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=158879; [1]
RN	SEQUENCE FROM N.A.
RP	SEQUENCE 21311952; PubMed=11418146;
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA	Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA	Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus
RT	"aureus.";
RL	Lancet 357;1225-1240(2001).
DR	EMBL; AF003364; BAB3119.1; -
DR	InterPro; IPR009229; AgrD.
DR	Pfam; PF05931; AgrD; 1.
KW	Complete proteome.
QY	SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
DB	24 GVNAXSLF 32
RESULT 4	
Q7A92745	PRELIMINARY; PRT; 47 AA.
ID	Q7A92745
AC	Q7A92745
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	AgrD protein.
GN	Name=agrD; OrderedLocusNames=SA1842.1; ORFNames=SA5066;
OS	Staphylococcus aureus (strain N315).
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=158879; [1]
RN	SEQUENCE FROM N.A.
RP	SEQUENCE 21311952; PubMed=11418146;
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA	Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA	Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus
RT	"aureus.";
RL	Lancet 357;1225-1240(2001).
DR	EMBL; AF003364; BAB3119.1; -
DR	InterPro; IPR009229; AgrD.
DR	Pfam; PF05931; AgrD; 1.
KW	Complete proteome.
QY	SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
DB	24 GVNAXSLF 32
RESULT 5	
Q7A92745	PRELIMINARY; PRT; 47 AA.
ID	Q7A92745
AC	Q7A92745
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	AgrD protein.
GN	Name=agrD; OrderedLocusNames=SA1842.1; ORFNames=SA5066;
OS	Staphylococcus aureus (strain N315).
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=158879; [1]
RN	SEQUENCE FROM N.A.
RP	SEQUENCE 21311952; PubMed=11418146;
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA	Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA	Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus
RT	"aureus.";
RL	Lancet 357;1225-1240(2001).
DR	EMBL; AF003364; BAB3119.1; -
DR	InterPro; IPR009229; AgrD.
DR	Pfam; PF05931; AgrD; 1.
KW	Complete proteome.
QY	SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
DB	24 GVNAXSLF 32
RESULT 6	
Q7A92745	PRELIMINARY; PRT; 47 AA.
ID	Q7A92745
AC	Q7A92745
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	AgrD protein.
GN	Name=agrD; OrderedLocusNames=SA1842.1; ORFNames=SA5066;
OS	Staphylococcus aureus (strain N315).
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.

RC STRAIN=gt36a-cp8;
 RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
 RT "Evolutionary Models for the Development of the Polymorphic Loci agr
 and cap in Staphylococcus aureus";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ617717; CA92751.1; -
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 84.6%; Score 33; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 5.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSALF 9
 |||||:|
 Db 24 GVNACSLF 32

RESULT 7

CAE92754 PRELIMINARY; PRT; 47 AA.
 AC CAE92754;
 DT 01-APR-2004 (TrEMBLrel. 27, Created)
 DT 01-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 01-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE AgRD protein.
 GN AGRD.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=gt36b-cp8;
 RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
 RT "Evolutionary Models for the Development of the Polymorphic Loci agr
 and cap in Staphylococcus aureus";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ617718; CA92754.1; -
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 84.6%; Score 33; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 5.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSALF 9
 |||||:|
 Db 24 GVNACSLF 32

RESULT 8

CAE92757 PRELIMINARY; PRT; 47 AA.
 AC CAE92757;
 DT 01-APR-2004 (TrEMBLrel. 27, Created)
 DT 01-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 01-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE AgRD protein.
 GN AGRD.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=gt11-cp8;
 RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
 RT "Evolutionary Models for the Development of the Polymorphic Loci agr
 and cap in Staphylococcus aureus";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ617719; CA92757.1; -
 SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 84.6%; Score 33; DB 2; Length 47;
 Best Local Similarity 77.8%; Pred. No. 5.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSALF 9
 |||||:|
 Db 24 GVNACSLF 32

RESULT 9

Q9FIUS PRELIMINARY; PRT; 46 AA.
 ID Q9FIUS;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE AgRD.
 GN Name=agrD;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21137858; PubMed=11240104;
 RA Takeuchi S., Maeda T., Hashimoto N., Imaizumi K., Kaidoh T.,
 RA Hayakawa Y.;
 RT "Variation of the agr locus in Staphylococcus aureus isolates from
 cows with mastitis";
 RL Vet. Microbiol. 79:267-274(2001).
 DR EMBL: AB043554; BAB18547.1; -
 DR InterPro; IPR009229; AgRD.
 DR Pfam; PF05931; AgRD; 1.
 DR PFAM; PF05931; AgRD; 1.
 SQ SEQUENCE 46 AA; 5050 MW; 404714CDC4BFA77E CRC64;

Query Match 82.1%; Score 32; DB 2; Length 46;
 Best Local Similarity 77.8%; Pred. No. 9.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSALF 9
 |||||:|
 Db 24 GVNACSLF 32

RESULT 10

Q922T9 PRELIMINARY; PRT; 189 AA.
 ID Q922T9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Lampl protein (Fragment).
 GN Name=Lampl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RX MEDLINE=2338257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 EN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RA TISSU=Brain;
 RA TISSU=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RC Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC006785; AA06785.1; -;
 DR MGI: 96745; Lamp1.
 DR GO: GO:0005764; C:lysosome; IDA.
 DR GO: GO:0005771; C:multivesicular body; IDA.
 DR GO: GO:0042383; C:sarcomatous; IDA.
 DR InterPro: IPR002000; Lamp.
 DR Pfam: PF01299; Lamp; 1.
 DR PRINTS: PR00336; LYSASSOCTDMP.
 DR PROSITE: PS00310; LAMP_1; 1.
 DR PROSITE: PS00311; LAMP_2; 1.
 FT NON TER 1
 FT SEQUENCE 189 AA; 20456 MW; 71F16D69BA4066FA CRC64;
 SQ

Query Match 82.1%; Score 32; DB 2; Length 189;
 Best Local Similarity 66.7%; Pred. No. 43;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 GVNAXSALF 9
 Db 63 GVNASSLF 71
 :||| :|||
 :||| :|||

RESULT 11
 LMP1_MOUSE STANDARD; PRT; 406 AA.
 AC P11438; Q62020;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (LGP-A)
 DE (LGP-120) (CD107A) (P2B)
 GN Name=Lamp1; Synonyms=Lamp-1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90307738; PubMed=2142158;
 RA Granger B.L., Green S.A., Gabel C.A., Howe C.L., Mellman I.,
 RA Helenius A.;
 RT "Characterization and cloning of lgp110, a lysosomal membrane
 RT glycoprotein from mouse and rat cells.";
 RL J. Biol. Chem. 265:12036-12043(1990).
 EN [2]
 RP SEQUENCE FROM N.A.
 RA Heffernan M., Yousefi S., Dennis J.W.;
 RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSU=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Sapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyik S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Mada A., Rodrigues S., Sanchez A.,
 RA Whiting M., Mada A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 EN [4]
 RP SEQUENCE OF 25-406 FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=88243732; PubMed=3379044;
 RA Chen J.W., Cha Y., Yusef K.U., Gracy R.W., August J.T.;
 RT "Isolation and sequencing of a cDNA clone encoding lysosomal membrane
 RT glycoprotein mouse LAMP-1. Sequence similarity to proteins bearing
 RT onco-differentiation antigens.";
 RL J. Biol. Chem. 263:8754-8758(1988).
 EN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=90237040; PubMed=2332434;
 RA Arterburn L.M., Barles B.J., August J.T.;
 RT "The disulfide structure of mouse lysosome-associated membrane protein
 RT 1.";
 RL J. Biol. Chem. 265:7419-7423(1990).
 CC -!- FUNCTION: Presents carbohydrate ligands to selectins. Also
 CC implicated in tumor cell metastasis.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal. This
 CC protein shuttles between lysosomes, endosomes, and the plasma
 CC membrane.
 CC -!- PTM: O- and N-glycosylated; some of the N-glycans attached to
 CC LAMP-1 are poly(lactosaminoglycans (by similarity)).
 CC -!- SIMILARITY: Belongs to the LAMP family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M32015; AAA39428.1; -;
 DR EMBL: M25244; AAA39869.1; -;
 DR EMBL: BC049097; AAA49097.1; -;
 DR EMBL: J03881; AAA39411.1; -;
 DR PIR: A28067; A28067.
 DR PIR: A60534; A60534.
 DR MGI: 96745; Lamp1.
 DR GO: GO:0005764; C:lysosome; IDA.
 DR InterPro: IPR002000; Lamp.
 DR Pfam: PF01299; Lamp; 1.
 DR PRINTS: PR00336; LYSASSOCTDMP.
 DR PROSITE: PS00310; LAMP_1; 2.
 DR PROSITE: PS00311; LAMP_2; 1.
 KW Direct protein sequencing; Glycoprotein; Lysosome; Signal;
 KW Transmembrane.
 FT SIGNAL 1 24
 FT CHAIN 25 406
 FT SIGNAL 1 24
 FT CHAIN 25 406
 FT -----
 FT Lysosome-associated membrane glycoprotein
 FT 1.
 FT DOMAIN 25 370
 FT TRANSMEM 371 394
 FT DOMAIN 395 406
 FT DOMAIN 25 189
 FT DOMAIN 189 218
 FT DOMAIN 219 370
 FT DISULFID 35 74
 FT DISULFID 149 185
 FT DISULFID 222 259
 FT DISULFID 327 364
 FT CARBOHYD 31 31
 FT CARBOHYD 52 52
 FT CARBOHYD 58 58
 FT -----
 FT N-linked (GLCNAC...) (Potential).
 FT N-linked (GLCNAC...) (Potential).
 FT N-linked (GLCNAC...) (Potential).

FT CARBOHYD 70 70 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 78 78 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 97 97 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 101 101 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 115 115 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 159 159 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 177 177 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 214 214 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 219 219 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 232 232 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 240 240 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 252 252 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 282 282 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 296 296 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 311 311 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 311 311 N-linked (GLCNAC...) (Potential).
 FT CONFLICT 1 10 MAAPGARRPL -> MRPPRAAV (in Ref. 2).
 FT CONFLICT 25 26 LF -> IP (in Ref. 4).
 FT CONFLICT 385 385 V -> I (in Ref. 2 and 4).
 SQ SEQUENCE 406 AA; 43865 MW; C1BD373548BB9655 CRC64;

Query Match 82.1%; Score 32; DB 1; Length 406;
 Best Local Similarity 66.7%; Pred. No. 98;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
 Db 280 GVNASSSLF 288

RESULT 12

ID Q8VH34 PRELIMINARY; PRT; 406 AA.
 AC Q8VH34;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE LAMP 1.
 GN Names=Lamp1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ono K., Han J.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY069968; AAL58070.1; -
 DR MGD; MGI:96745; Lamp1.
 DR GO; GO:0005764; C:lysosome; IDA.
 DR GO; GO:0005771; C:multivesicular body; IDA.
 DR GO; GO:0042383; C:sarcolemma; IDA.
 DR InterPro; IPR002000; Lamp.
 DR Pfam; PF01299; Lamp; 1.
 DR PRINTS; PR00336; LYSASSOCTDMP.
 DR PROSITE; PS00310; LAMP_1; 2.
 DR PROSITE; PS00311; LAMP_2; 1.
 SQ SEQUENCE 406 AA; 43879 MW; C1BD373548ADFA55 CRC64;

Query Match 82.1%; Score 32; DB 2; Length 406;
 Best Local Similarity 66.7%; Pred. No. 98;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSALF 9
 Db 280 GVNASSSLF 288

RESULT 13

ID LMPI_RAT STANDARD; PRT; 407 AA.
 AC P14562; P97620;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (120
 kDa lysosomal membrane glycoprotein) (LGP-120) (CD107A).
 GN Name=Lamp1; Synonyms=Lamp-1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=89017240; PubMed=3174652;
 RA Howe C.L., Granger B.L., Hull M., Green S.A., Gabel C.A., Helenius A.,
 Mellman I.,
 RT "Derived protein sequence, oligosaccharides, and membrane insertion of
 the 120-kDa lysosomal membrane glycoprotein (lgp120): identification
 of a highly conserved family of lysosomal membrane glycoproteins.";
 RT Proc. Natl. Acad. Sci. U.S.A. 85:7577-7581(1988).
 RL FEBS Lett. 244:351-356(1989).
 RN [3]
 RP SEQUENCE OF 22-407 FROM N.A.
 MEDLINE=89153580; PubMed=2920835;
 RA Himeno M., Noguchi Y., Sasaki H., Tanaka Y., Furuno K., Kono A.,
 Sakaki Y., Kato K.;
 RT "Isolation and sequencing of a cDNA clone encoding 107 kDa
 sialoglycoprotein in rat liver lysosomal membranes.";
 RL FEBS Lett. 244:351-356(1989).
 RN [3]
 RP SEQUENCE OF 283-357 FROM N.A.
 STRAIN=Wistar Kyoto; Tissue=Aortic smooth muscle;
 RA Adams L.A., Werny I., Schwartz S.M.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Presents carbohydrate ligands to selectins. Also
 implicated in tumor cell metastasis.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal. This
 protein shuttles between lysosomes, endosomes, and the plasma
 membrane.
 CC -!- PTM: O- and N-glycosylated; some of the N-glycans attached to
 LAMP-1 are poly(N-acetylglucosamine) (By similarity).
 CC -!- SIMILARITY: Belongs to the LAMP family.
 CC
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 EMBL; M34559; AAA41525.1; -
 DR EMBL; X14765; CAA32873.1; -
 DR EMBL; U75406; AAB19108.1; -
 DR PIR; A30200; A30200.
 DR RGD; 2989; Lamp1.
 DR InterPro; IPR002000; Lamp.
 DR Pfam; PF01299; Lamp; 1
 DR PRINTS; PR00336; LYSASSOCTDMP.
 DR PROSITE; PS00310; LAMP_1; 2.
 DR PROSITE; PS00311; LAMP_2; 1.
 KW Glycoprotein; Lysosome; Signal; Transmembrane.
 FT SIGNAL 1 21
 FT CHAIN 22 407 Lysosome-associated membrane glycoprotein
 1.
 FT DOMAIN 22 371 Luminal (Potential).
 FT TRANSMEM 372 395 Potential.
 FT DOMAIN 396 407 Cytoplasmic (Potential).
 FT DOMAIN 22 189 First luminal domain.
 FT DOMAIN 190 219 Hinge.
 FT DOMAIN 220 371 Second luminal domain.
 FT DISULFID 36 75 By similarity.
 FT DISULFID 150 186 By similarity.
 FT DISULFID 223 260 By similarity.
 FT DISULFID 328 365 By similarity.
 FT CARBOHYD 32 32 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).

CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC Preliminary data.

DR EMBL; AABF01000023; EAA24592.1; -;
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0008769; F:X-His dipeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001261; ARGE_dapE_M20.
 DR InterPro; IPR002933; Peptidase_M20.
 DR InterPro; IPR010964; Pept_M20A_pepv.
 DR Pfam; PF01546; Peptidase_M20; 1.
 DR TIGRFAMs; TIGR01887; dipeptidase-like; 1.
 DR PROSITE; PS00758; ARGE_DAPE_CPG2_1; UNKNOWN_1.
 KW Dipeptidase; Hydrolase
 SQ SEQUENCE 452 AA; 50268 MW; 8F64B0ACBE9406FA CRC64;

Query Match 82.1%; Score 32; DB 2; Length 452;
 Best Local Similarity 77.8%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYNAXSALF 9
 | | | | |
 Db 260 GYNAVSALF 268

Search completed: October 26, 2004, 16:05:05
 Job time : 42.6324 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:15 ; Search time 42.75 Seconds
(without alignments)
75.522 Million cell updates/sec

Title: US-10-032-950-7

Perfect score: 39

Sequence: 1 GVXAXSAF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	94.9	9	3 AAY67857	Aay67857 S. aureus
2	37	94.9	9	5 RAM50905	Ram50905 AgrD-auto
3	37	94.9	9	5 ABP53546	Abp53546 Cyclic pe
4	33	84.6	9	3 AAY67860	Aay67860 Staphyloc
5	33	84.6	9	3 AAY67859	Aay67859 Staphyloc
6	33	84.6	9	5 ABB07160	Abb07160 Peptide-m
7	33	84.6	9	5 RAM50907	Ram50907 Protected
8	33	84.6	9	5 RAM51004	Ram51004 AgrD2 lac
9	33	84.6	9	5 RAM51003	Ram51003 AgrD2 lin
10	33	84.6	9	5 RAM51002	Ram51002 AgrD2 lin
11	32	82.1	9	3 AAY67851	Aay67851 S. aureus
12	32	82.1	9	3 AAY67861	Aay67861 Staphyloc
13	32	82.1	9	5 ABB07161	Abb07161 Peptide-m
14	32	82.1	9	5 RAM51005	Ram51005 AgrD2 lac
15	32	82.1	9	5 RAM50908	Ram50908 Protected
16	32	82.1	9	5 RAM50899	Ram50899 AgrD-auto
17	32	82.1	9	5 ABP53540	Abp53540 Cyclic pe
18	31	79.5	9	2 AAW38323	Aaw38323 Transcrip
19	31	79.5	9	5 ABB07159	Abb07159 Peptide-m
20	31	79.5	9	5 RAM51001	Ram51001 AgrD2 thi
21	31	79.5	9	6 ABB84631	Abb84631 S. aureus
22	31	79.5	9	7 ADF09190	Adf09190 S. aureus
23	31	79.5	9	8 ADJ98875	Adj98875 Peptide t
24	31	79.5	47	6 ABB84634	Abb84634 S. aureus
25	31	79.5	47	7 ADF09193	Adf09193 S. aureus

26	31	79.5	277	7	ABO66477	AbO66477 Klebsiell
27	31	79.5	924	6	ABU02122	Abu02122 S. pneumo
28	31	79.5	924	8	ADK46701	Adk46701 Streptoco
29	31	79.5	924	8	ADM92204	Adm92204 S. pneumo
30	30	76.9	163	5	ABU05504	Abu05504 M. tuberc
31	30	76.9	167	5	ABU05887	Abu05887 M. tuberc
32	30	76.9	167	6	ABP57498	Abp57498 Mycobacte
33	30	76.9	311	7	ADJ69797	Adj69797 Human hea
34	30	76.9	416	2	AAR69554	Aar69554 Human lys
35	30	76.9	416	3	AAY52550	Aay52550 Human lys
36	30	76.9	416	7	ADP65283	Adp65283 Human lys
37	30	76.9	416	8	ADN03755	Adn03755 Antipsoxi
38	30	76.9	416	8	ADP49321	Adp49321 Human lys
39	30	76.9	417	2	AAR01940	Aar01940 Tumour ne
40	30	76.9	614	5	AAU09996	Aau09996 Genticulo
41	30	76.9	614	5	AAQ78515	Aaq78515 Haloperox
42	30	76.9	945	4	ABB60000	Abb60000 Drosophil
43	29	74.4	9	3	AAY67855	Aay67855 S. aureus
44	29	74.4	9	3	AAY67856	Aay67856 S. aureus
45	29	74.4	9	5	AAM50903	Aam50903 AgrD-auto

ALIGNMENTS

RESULT 1
AAY67857
ID AAY67857 standard; peptide; 9 AA.
XX
AC AAY67857;
XX
DT 25-APR-2000 (first entry)
XX
DE S. aureus peptide #6 used for bacterial interference.
XX
KW Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;
KW virulence factor; treatment.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal residue forms bond with C-terminal
FT residue to form a cyclic peptide"
FT Misc-difference 5
FT /label= Unknown
XX
PN WO9967286-A2.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-US014562.
XX
PR 24-JUN-1999; 98US-00103438.
XX
PA (UYRQ) UNIV ROCKEFELLER.
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Muir TW, Mayville P, Novick RP, Ji G, Beavis R;
DR WPI; 2000-147202/13.
XX
PT New cyclic peptides for treating infections with Staphylococcus aureus.
PS Claim 9; Page 26; 37pp; English.
XX
CC This sequence represents a cyclic peptide derived from the Staphylococcus
CC aureus AgrD peptide. The invention relates to AgrD derived peptides, a
CC composition containing a peptide and a carrier, and a method for the
CC production of the cyclic peptides. The peptide inhibits the agr response,
CC which is normally associated with the release of virulence factors of
CC Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
CC activates the agr response in strains of a single group, but interferes

CC with this response in strains of different groups. The peptides and
CC composition containing them can be used to treat infections by *S. aureus*
XX
SQ Sequence 9 AA;
Query Match 94.9%; Score 37; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GVNAXSSAF 9
DB 1 GVNAXSSAF 9
RESULT 2
AAM50905
ID AAM50905 standard; peptide; 9 AA.
XX
AC AAM50905;
XX
DT 08-MAY-2002 (first entry)
DE AgrD-autoinducing cyclic peptide, inhibitor of agr response.
XX
KW Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
KW antibacterial; infection; therapy; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 5
FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"
FT Misc-difference 9 /note= "any amino acid"
FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"
XX
PN US6337385-B1.
XX
PD 08-JAN-2002.
XX
PF 24-JUN-1999; 99US-00339511.
XX
PR 24-JUN-1998; 98US-0090402P.
XX
PA (UYRQ) UNIV ROCKEFELLER.
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX WPI; 2002-170774/22.
XX
PT Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
FT interference and for treating Staphylococcus aureus infection in a
FT subject.
XX
PS Claim 7; Col 19; 18pp; English.
XX
CC The present sequence is that of a novel synthetic cyclic peptide of the
CC invention that is capable of inhibiting the agr response of
CC Staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is
CC a secreted agr-encoded peptide and where the agr locus controls the
CC synthesis of virulence factor and other extracellular proteins
CC responsible for pathogenicity in *S. aureus*. Preferred peptides may have
CC the sequence NH₂-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z
CC residue and COOH other than a thioester bond, where X is an amino acid,
CC an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a
CC synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The
CC cyclic bond is especially a lactam or lactone bond. The thiololactone
CC structure within native AgrD peptides is required for activation of the
CC agr response. Elimination of the thiol ester component of the cyclic ring
CC structure can destroy agr response activating activity while preserving
CC and enhancing inhibitory activity. A claimed method of preparing a cyclic

CC peptide involves: assembling a linear peptide chain on to a solid phase
CC resin support; deprotecting the resulting protected assembled peptide;
CC treating the deprotected peptide with neutral buffer for a time
CC sufficient to form the cyclic peptide and cleave the peptide from the
CC support; and recovering the cyclic peptide. The peptide is useful for
CC bacterial interference, especially for the treatment of *S. aureus*
CC infection
XX
SQ Sequence 9 AA;
Query Match 94.9%; Score 37; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GVNAXSSAF 9
DB 1 GVNAXSSAF 9
RESULT 3
ABP53546
ID ABP53546 standard; peptide; 9 AA.
XX
AC ABP53546;
XX
DT 13-DEC-2002 (first entry)
DE Cyclic peptide SEQ ID NO:7.
XX
KW Cyclic peptide; Staphylococcus aureus; infection; antibacterial;
KW agr response inhibitor.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 5 /note= "any amino acid"
FT Misc-difference 5
XX
PN US2002077453-A1.
XX
PD 20-JUN-2002.
XX
PF 27-DEC-2001; 2001US-00032950.
XX
PR 24-JUN-1998; 98US-0090402P.
PR 24-JUN-1999; 99US-00339511.
XX
PA (MUIR/) MUIR T W.
PA (MAYV/) MAYVILLE P.
PA (NOVI/) NOVICK R P.
PA (BEAV/) BEAVIS R.
PA (JIGG/) JI G.
XX
PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX WPI; 2002-681366/73.
XX
PT New cyclic peptides, useful for treating Staphylococcus aureus
FT infections.
XX
PS Claim 9; Page 10; 18pp; English.
XX
CC ABP53540 to ABP53547 represent cyclic peptides (I) from the present
CC invention. The present invention also describes a method for treating
CC Staphylococcus aureus infection comprising the administration of a
CC composition comprising (I). (I) has antibacterial activity, and can be
CC used as an agr gene response inhibitor. The peptides are useful for
CC treating *S. aureus* infections
XX
SQ Sequence 9 AA;
Query Match 94.9%; Score 37; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVNAXSSAF 9
Db 1 GVNAXSSAF 9

RESULT 4
AAy67860
ID AAY67860 standard; peptide; 9 AA.
AC AAY67860;
XX
XX 25-APR-2000 (first entry)
XX
XX Staphylococcus aureus AgrDII derived peptide sequence.
DE
XX Staphylococcus aureus infection; AgrD; agr response; treatment;
KW virulence factor.
XX
XX Staphylococcus aureus.
OS
XX WO9967286-A2.
FN
XX 29-DEC-1999.
XX
XX 24-JUN-1999; 99WO-US014562.
PF
XX 24-JUN-1998; 98US-00103438.
PR
XX (UYRQ ) UNIV ROCKEFELLER.
PA (UYNV ) UNIV NEW YORK STATE.
XX
XX Muir TW, Mayville P, Novick RP, Ji G, Beavis R;
PI WPI; 2000-147202/13.
XX
XX New cyclic peptides for treating infections with Staphylococcus aureus.
DR
XX Example; Page 22; 37pp; English.
XX
XX This sequence represents the Staphylococcus aureus AgrDII derived
CC peptide. The invention relates to AgrD derived cyclic peptides, a
CC composition containing a peptide and a carrier, and a method for the
CC production of the cyclic peptides. The peptide inhibits the agr response,
CC which is normally associated with the release of virulence factors of
CC Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
CC activates the agr response in strains of a single group, but interferes
CC with this response in strains of different groups. The peptides and
CC composition containing them can be used to treat infections by S. aureus
XX
XX Sequence 9 AA;
SQ

Query Match 84.6%; Score 33; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSSAF 9
Db 1 GVNAXSSAF 9

RESULT 6
ABB07160
ID ABB07160 standard; peptide; 9 AA.
XX
XX ABB07160;
AC
XX 13-MAR-2002 (first entry)
DT
XX
XX Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
DE
XX Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
XX vulnery; pheromone; agr system; accessory gene regulator; cyclic.
KW
XX Synthetic.
OS
XX WO200185664-A2.
XX
XX 15-NOV-2001:
PD
XX
XX 10-MAY-2001; 2001WO-US015221.
PF
XX
XX 10-MAY-2000; 2000US-0203000P.
PR
XX 07-DEC-2000; 2000US-0254398P.
XX
XX (UYPR-) UNIV PRINCETON.
PA (QUOR-) QUOREX PHARM INC.
XX (UYTE-) UNIV TECHNOLOGIES INT INC.
PA
XX
XX Bassler BL, Dammel CS, Schauder S, Shokat K, Stein J, Surette MG;
PI

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```

virulence factor.
XX
XX Staphylococcus aureus.
OS
XX WO9967286-A2.
PN
XX
XX 29-DEC-1999.
PD
XX
XX 24-JUN-1999; 99WO-US014562.
PF
XX 24-JUN-1998; 98US-00103438.
PR
XX (UYRQ ) UNIV ROCKEFELLER.
PA (UYNV ) UNIV NEW YORK STATE.
XX
XX Muir TW, Mayville P, Novick RP, Ji G, Beavis R;
PI WPI; 2000-147202/13.
XX
XX New cyclic peptides for treating infections with Staphylococcus aureus.
DR
XX Example; Page 22; 37pp; English.
XX
XX This sequence represents the Staphylococcus aureus AgrDII derived
CC peptide. The invention relates to AgrD derived cyclic peptides, a
CC composition containing a peptide and a carrier, and a method for the
CC production of the cyclic peptides. The peptide inhibits the agr response,
CC which is normally associated with the release of virulence factors of
CC Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
CC activates the agr response in strains of a single group, but interferes
CC with this response in strains of different groups. The peptides and
CC composition containing them can be used to treat infections by S. aureus
XX
XX Sequence 9 AA;
SQ

Query Match 84.6%; Score 33; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSSAF 9
Db 1 GVNAXSSAF 9

RESULT 6
ABB07160
ID ABB07160 standard; peptide; 9 AA.
XX
XX ABB07160;
AC
XX 13-MAR-2002 (first entry)
DT
XX
XX Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
DE
XX Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
XX vulnery; pheromone; agr system; accessory gene regulator; cyclic.
KW
XX Synthetic.
OS
XX WO200185664-A2.
XX
XX 15-NOV-2001:
PD
XX
XX 10-MAY-2001; 2001WO-US015221.
PF
XX
XX 10-MAY-2000; 2000US-0203000P.
PR
XX 07-DEC-2000; 2000US-0254398P.
XX
XX (UYPR-) UNIV PRINCETON.
PA (QUOR-) QUOREX PHARM INC.
XX (UYTE-) UNIV TECHNOLOGIES INT INC.
PA
XX
XX Bassler BL, Dammel CS, Schauder S, Shokat K, Stein J, Surette MG;
PI

```

XX DR WPI; 2002-075235/10.
 XX PT Use of autoinducer-2 agonists or antagonists for regulating activity of
 XX PT autoinducer-2 receptor; regulating bacterial growth and pathogenesis,
 XX PT also antibiotic compositions.
 XX PS Disclosure; Page 33; 134pp; English.
 XX CC The invention relates to the use of autoinducer-2 (AI-2) agonists or
 XX CC antagonists for regulating activity of autoinducer-2 receptor, regulating
 XX CC bacterial growth and pathogenesis. Synergistic antibiotic compositions
 XX CC comprising inhibitors of the quorum-sensing pathway of a microorganism
 XX CC are also provided. Methods using such AI-2 analogues are useful for
 XX CC treating pathogen-associated disease states. The compounds and antibiotic
 XX CC compositions can be used to inhibit bacterial cell growth and/or biofilm
 XX CC formation on a medical device, particularly for promoting growth of skin
 XX CC graft replacements used in the treatment of burns and ulcers. They may
 XX CC also be used to aid wound repair, and to inhibit bacterial cell growth
 XX CC and biofilm formation in or on products or devices used for personal
 XX CC hygiene. The present sequence represents a inhibitor of peptide-mediated
 XX CC quorum sensing
 XX SQ Sequence 9 AA;
 Query Match 84.6%; Score 33; DB 5; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GVNAXSSAF 9
 |||||
 DB 1 GVNASSSLF 9

RESULT 7
 AAM50907
 ID AAM50907 standard; peptide; 9 AA.
 XX AC AAM50907;
 XX DT 08-MAY-2002 (first entry)
 XX DE Protected peptide used in cyclic peptide production.
 XX KW Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
 XX KW antibacterial; infection; therapy; cyclic.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 1
 XX FT /note= "Z-Gly"
 XX FT Misc-difference 5
 XX FT /note= "note linked to residue 9 to form cyclic peptide"
 XX FT Modified-site 5
 XX FT /note= "Ser(-tBu)"
 XX FT Modified-site 6
 XX FT /note= "Ser(Bzl)"
 XX FT Modified-site 7
 XX FT /note= "Ser(Bzl)"
 XX FT Misc-difference 9
 XX FT /note= "note linked to residue 5 to form cyclic peptide"
 XX FT
 XX PN USG337385-B1.
 XX XX 08-JAN-2002.
 XX PD
 XX PF 24-JUN-1999; 99US-00339511.
 XX PR 24-JUN-1998; 98US-0090402P.
 XX PA (UYRQ) UNIV ROCKEFELLER.
 XX PA (UTNY) UNIV NEW YORK STATE.

XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
 XX DR WPI; 2002-170774/22.
 XX PT Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 XX PT interference and for treating Staphylococcus aureus infection in a
 XX PT subject.
 XX PS Disclosure; Col 14; 18pp; English.
 XX CC The present sequence is that of a protected peptide used in an example of
 XX CC the preparation of novel synthetic cyclic peptides of the invention (see
 XX CC AAM5099-306). The peptide corresponds to the Staphylococcus aureus
 XX CC AgrDII sequence with a Cys5 to Ser mutation (lactone). It was synthesised
 XX CC on a Wang-resin using an Fmoc N-alpha protection strategy. Following
 XX CC chain assembly, the peptide was cleaved from the support and the Ser-5
 XX CC residue deprotected by treatment with a trifluoroacetic
 XX CC acid:anisole:water mixture (90:5:5) for 4 hr. The partially protected
 XX CC peptide-alpha carboxylates were then dissolved in DMF and treated with
 XX CC PyBOP and a catalytic amount of dimethylaminopyridine. Cyclization was
 XX CC complete after 2 hr. The remaining protecting groups were then removed by
 XX CC treatment with HF and the peptide purified by HPLC. The cyclic peptide is
 XX CC capable of inhibiting the agr response of Staphylococcus aureus. The
 XX CC thiolactone structure within native AgrD peptides is required for
 XX CC activation of this response. Replacement of the thiol ester component of
 XX CC the cyclic ring structure with a lactone (as in the present case) or a
 XX CC lactam can destroy agr response activating activity while preserving and
 XX CC enhancing inhibitory activity. The cyclic peptides are useful for
 XX CC bacterial interference, especially for the treatment of S. aureus
 XX CC infection
 XX SQ Sequence 9 AA;
 Query Match 84.6%; Score 33; DB 5; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GVNAXSSAF 9
 |||||
 DB 1 GVNASSSLF 9

RESULT 8
 AAM51004
 ID AAM51004 standard; peptide; 9 AA.
 XX AC AAM51004;
 XX DT 07-AUG-2003 (revised)
 XX DT 08-MAY-2002 (first entry)
 XX DE AgrD2 lactone cyclic peptide.
 XX KW AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
 XX KW therapy; lactone; cyclic.
 XX OS Staphylococcus aureus.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 5
 XX FT /note= "note linked to residue 9 to form cyclic peptide"
 XX FT Misc-difference 9
 XX FT /note= "note linked to residue 5 to form cyclic peptide"
 XX FT
 XX PN USG337385-B1.
 XX XX 08-JAN-2002.
 XX PD
 XX PF 24-JUN-1999; 99US-00339511.
 XX PR 24-JUN-1998; 98US-0090402P.
 XX PA (UYRQ) UNIV ROCKEFELLER.
 XX PA (UTNY) UNIV NEW YORK STATE.

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XX (UYRQ ) UNIV ROCKEFELLER.
PA (UYNY ) UNIV NEW YORK STATE.
XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX WPI; 2002-170774/22.
XX
XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
PT interference and for treating Staphylococcus aureus infection in a
PT subject.
XX
XX Example 1; Col 9; 18pp; English.
XX
XX The present sequence is that of a novel synthetic AgrD2 linear free acid
CC peptide in which residue 5 of the peptide is linked to residue 9 via a
CC lactone bond. The peptide is derived from an AgrD2 peptide of
CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
CC where the agr locus controls the synthesis of virulence factor and other
CC extracellular proteins responsible for pathogenicity in S. aureus. The
CC biological activity of the synthetic peptide was assayed using cultured
CC S. aureus strains containing a beta-lactamase reporter gene fused to the
CC agrP3 promoter. This allowed activation or inhibition of the agr response
CC to be monitored spectrophotometrically. The lactone AgrD2 peptide
CC inhibited the agr response in group I, II or III strains. The invention
CC activates claimed cyclic peptides (see AAMS0899-906 and AAMS0999) and
CC provides methods for preparing them, especially peptides where the cyclic bond is
CC a lactam or lactone bond. The cyclic peptides are useful for bacterial
CC interference, especially for the treatment of S. aureus infection.
XX (Updated on 07-AUG-2003 to correct OS field.)
XX
XX Sequence 9 AA;
SQ
Query Match 84.6%; Score 33; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GVNAXSSAF 9
DB 1 GVNASSSLF 9
RESULT 9
AAMS1003
ID AAMS1003 standard; peptide; 9 AA.
AC AAMS1003;
XX 08-MAY-2002 (first entry)
XX AgrD2 linear free acid peptide.
XX AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
XX therapy.
XX Staphylococcus aureus.
XX Synthetic.
XX US6337385-B1.
XX 08-JAN-2002.
XX 24-JUN-1999; 99US-00339511.
XX 24-JUN-1998; 98US-0090402P.
XX (UYRQ ) UNIV ROCKEFELLER.
XX (UYNY ) UNIV NEW YORK STATE.
XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX WPI; 2002-170774/22.
XX
XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
PT interference and for treating Staphylococcus aureus infection in a
PT subject.
XX
XX Example 1; Col 9; 18pp; English.
XX
XX The present sequence is that of a novel synthetic AgrD2 linear free acid
CC peptide. The peptide is derived from the cyclic AgrD2 peptide of
CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
CC where the agr locus controls the synthesis of virulence factor and other
CC extracellular proteins responsible for pathogenicity in S. aureus. The
CC biological activity of the synthetic peptide was assayed using cultured
CC S. aureus strains containing a beta-lactamase reporter gene fused to the
CC agrP3 promoter. This allowed activation or inhibition of the agr response
CC to be monitored spectrophotometrically. Unlike an AgrD2 thiolactone
CC cyclic peptide (see AAMS1001), the present peptide was unable to either
CC activate or inhibit the agr response, even when added to cultured cells
CC at uM concentrations. The invention provides claimed cyclic peptides (see
CC AAMS0899-906 and AAMS0999) and methods for preparing them. The cyclic
CC peptides are useful for bacterial interference, especially for the
XX treatment of S. aureus infection
XX
XX Sequence 9 AA;
SQ
Query Match 84.6%; Score 33; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GVNAXSSAF 9
DB 1 GVNASSSLF 9
RESULT 10
AAMS1002
ID AAMS1002 standard; peptide; 9 AA.
XX AAMS1002;
XX AC
XX 08-MAY-2002 (first entry)
XX AgrD2 linear thioester peptide.
XX AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
XX therapy.
XX Staphylococcus aureus.
XX Synthetic.
XX Key Location/Qualifiers
FT Modified-site 9 /note= "C-terminal thioester"
XX US6337385-B1.
XX 08-JAN-2002.
XX 24-JUN-1999; 99US-00339511.
XX 24-JUN-1998; 98US-0090402P.
XX (UYRQ ) UNIV ROCKEFELLER.
XX (UYNY ) UNIV NEW YORK STATE.
XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
XX WPI; 2002-170774/22.
XX
XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
PT interference and for treating Staphylococcus aureus infection in a
PT subject.
XX
XX WPI; 2002-170774/22.

```

PS Example 1; Col 9; 18pp; English.

XX The present sequence is that of a novel synthetic AgrD2 linear thioester
CC peptide. The peptide is derived from the cyclic AgrD2 peptide of
CC Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide,
CC where the agr locus controls the synthesis of virulence factor and other
CC extracellular proteins responsible for pathogenicity in *S. aureus*. The
CC biological activity of the synthetic peptide was assayed using cultured
CC *S. aureus* strains containing a beta-lactamase reporter gene fused to the
CC agrP3 promoter. This allowed activation or inhibition of the agr response
CC to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone
CC cyclic peptide (see AM51001), the present peptide was unable to either
CC activate or inhibit the agr response, even when added to cultured cells
CC at uM concentrations. The invention provides claimed cyclic peptides (see
CC AM50899-906 and AM50999) and methods for preparing them. The cyclic
CC peptides are useful for bacterial interference, especially for the
CC treatment of *S. aureus* infection

XX Sequence 9 AA;

Query Match 84.6%; Score 33; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
Db 1 GVNAXSSLF 9

RESULT 11

AAAY67851 standard; peptide; 9 AA.

AC AAAY67851;

XX 25-APR-2000 (first entry)

XX *S. aureus* peptide #1 used for bacterial interference.

XX Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;
KW virulence factor; treatment.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Misc-difference 5 /label= Unknown

XX WO9967286-A2.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-US014562.

XX 24-JUN-1998; 98US-00103438.

XX (UVRQ) UNIV ROCKEFELLER.

XX (UVRQ) UNIV NEW YORK STATE.

XX Muir TW, Mayville P; Novick RP, Ji G, Beavis R;

XX WPI; 2000-147202/13.

XX New cyclic peptides for treating infections with Staphylococcus aureus.

PS Claim 9; Page 26; 37pp; English.

XX This sequence represents a cyclic peptide derived from the Staphylococcus
CC aureus AgrD peptide. The invention relates to AgrD derived peptides, a
CC composition containing a peptide and a carrier, and a method for the
CC production of the cyclic peptides. The peptide inhibits the agr response,
CC which is normally associated with the release of virulence factors of
CC Staphylococcus aureus. An AgrD peptide is produced by *S. aureus* that

CC activates the agr response in strains of a single group, but interferes
CC with this response in strains of different groups. The peptides and
CC composition containing them can be used to treat infections by *S. aureus*

XX Sequence 9 AA;

Query Match 82.1%; Score 32; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9

Db 1 GVNAXSSLF 9

RESULT 12

AAAY67861 standard; peptide; 9 AA.

XX AAAY67861;

XX 25-APR-2000 (first entry)

XX Staphylococcus aureus AgrDII derived peptide sequence.

XX Staphylococcus aureus infection; AgrD; agr response; treatment;
KW virulence factor.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Misc-difference 5 /label= Unknown

XX WO9967286-A2.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-US014562.

XX 24-JUN-1998; 98US-00103438.

XX (UVRQ) UNIV ROCKEFELLER.

XX (UVRQ) UNIV NEW YORK STATE.

XX Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX WPI; 2000-147202/13.

XX New cyclic peptides for treating infections with Staphylococcus aureus.

PS Example; Page 22; 37pp; English.

XX This sequence represents the Staphylococcus aureus AgrDII derived
CC peptide. The invention relates to AgrD derived cyclic peptides, a
CC composition containing a peptide and a carrier, and a method for the
CC production of the cyclic peptides. The peptide inhibits the agr response,
CC which is normally associated with the release of virulence factors of
CC Staphylococcus aureus. An AgrD peptide is produced by *S. aureus* that
CC activates the agr response in strains of a single group, but interferes
CC with this response in strains of different groups. The peptides and
CC composition containing them can be used to treat infections by *S. aureus*

XX Sequence 9 AA;

Query Match 82.1%; Score 32; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9

Db 1 GVNAXSSLF 9

XX AC AAM50908;
 XX DT 08-MAY-2002 (first entry)
 XX DE Protected peptide used in cyclic peptide production.
 XX KW Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
 XX KW antibacterial; infection; therapy; cyclic.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 XX FT Modified-site 1 /note= "Z-Gly"
 XX FT Misc-difference 5 /note= "note linked to residue 9 to form cyclic peptide"
 XX FT Modified-site 5 /label= Dpr(Boc)
 XX FT Modified-site 6 /note= "Ser(Bzl)"
 XX FT Modified-site 7 /note= "Ser(Bzl)"
 XX FT Misc-difference 9 /note= "note linked to residue 5 to form cyclic peptide"
 XX PN US6337385-B1.
 XX PD 08-JAN-2002.
 XX PF 24-JUN-1999; 99US-00339511.
 XX PR 24-JUN-1998; 98US-0090402P.
 XX PA (UYRO) UNIV ROCKEFELLER.
 XX PA (UINY) UNIV NEW YORK STATE.
 XX PI Muir TW, Mayville P, Novick RP, Beavis R, Ji G;
 XX DR WPI; 2002-170774/22.
 XX PT Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 XX PT interference and for treating Staphylococcus aureus infection in a
 XX PT subject.
 XX PS Disclosure; Col 14; 18pp; English.
 XX CC The present sequence is that of a protected peptide used in an example of
 XX CC the preparation of novel synthetic cyclic peptides of the invention (see
 XX CC AAM50899-906). The peptide corresponds to the Staphylococcus aureus
 XX CC AgrDII sequence with a Cys5 to diaminopropionic acid (Dpr) mutation
 XX CC (lactam). It was synthesised on a Wang-resin using an Fmoc N-alpha
 XX CC protection strategy. Following chain assembly, the peptide was cleaved
 XX CC from the support and the Dpr-5 residue deprotected by treatment with a
 XX CC trifluoroacetic acid:aniso:water mixture (90:5:5) for 4 hr. The
 XX CC partially protected peptide-alpha carboxylates were then dissolved in DMF
 XX CC and treated with PyBOP. Cyclization was complete after 2 hr. The
 XX CC remaining protecting groups were removed by treatment with HF and the
 XX CC peptide purified by HPLC. The cyclic peptide is capable of inhibiting the
 XX CC agr response of Staphylococcus aureus. The thiolactone structure within
 XX CC native AgrD peptides is required for activation of this response.
 XX CC Replacement of the thiol ester component of the cyclic ring structure
 XX CC with a lactam (as in the present case) or a lactone can destroy agr
 XX CC response activating activity while preserving and enhancing inhibitory
 XX CC activity. The cyclic peptides are useful for bacterial interference,
 XX CC especially for the treatment of S. aureus infection
 XX SQ Sequence 9 AA;

Query Match 82.1%; Score 32; DB 5; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GVNAXSSAF 9
 Db 1 GVNAXSSLF 9

Search completed: October 26, 2004, 15:59:46
 Job time : 43.75 secs

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:54:00 ; Search time 31.5 Seconds
(without alignments)
92.502 Million cell updates/sec

Title: US-10-032-950-7

Perfect score: 39

Sequence: 1 GVNAXSSAF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	32	82.1	9	13	US-10-032-950-1
3	32	82.1	112	15	US-10-424-599-260065
4	31	79.5	19	14	US-10-201-444-3
5	31	79.5	47	14	US-10-201-444-6
6	31	79.5	54	15	US-10-424-599-181018
7	30	76.9	136	15	US-10-424-599-272035
8	30	76.9	163	14	US-10-080-170-155
9	30	76.9	163	16	US-10-080-170-155
10	30	76.9	163	17	US-10-468-356-155
11	30	76.9	167	14	US-10-080-170-538
12	30	76.9	167	16	US-10-080-170-538
13	30	76.9	167	17	US-10-468-356-538

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76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	
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ALIGNMENTS

RESULT 1

US-10-032-950-7
; Sequence 7, Application US/10032950
; Publication NO. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032, 950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090, 402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-7

Query Match 94.9%; Score 37; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9

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Db          1  GVNAXSSAF 9
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; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-1
Query Match      82.1%; Score 32; DB 13; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GVNAXSSAF 9
|||||||
Db          1  GVNAXSSSLF 9

RESULT 3
US-10-424-599-260065
; Sequence 260065, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 260065
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_76863C.1.pap
US-10-424-599-260065
Query Match      82.1%; Score 32; DB 15; Length 112;
Best Local Similarity 66.7%; Pred. No. 18;
Matches      6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  GVNAXSSAF 9
|:|:|:|:|

US-10-032-950-7.rapb
Db          2  GINGISSAF 10
|||||||
RESULT 4
US-10-201-444-3
; Sequence 3, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT APPLICATION NUMBER: US/10/201,444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-3
Query Match      79.5%; Score 31; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches      7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GVNAXSSAF 9
|||||||
Db          1  GVNACSSLF 9

RESULT 5
US-10-201-444-6
; Sequence 6, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT APPLICATION NUMBER: US/10/201,444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-6
Query Match      79.5%; Score 31; DB 14; Length 47;
Best Local Similarity 77.8%; Pred. No. 12;
Matches      7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GVNAXSSAF 9
|||||||
Db          24  GVNACSSLF 32

RESULT 6
US-10-424-599-181018
; Sequence 181018, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
US-10-424-599-181018
Query Match      82.1%; Score 32; DB 15; Length 112;
Best Local Similarity 66.7%; Pred. No. 18;
Matches      6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  GVNAXSSAF 9
|:|:|:|:|
```

```
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 181018
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_134473C.1.pep
US-10-424-599-181018

Query Match      79.5%; Score 31; DB 15; Length 54;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSA 8
DB 47 GVNAXSSA 54

RESULT 7
US-10-424-599-272035
; Sequence 272035, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 272035
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(136)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_87667C.1.pep
US-10-424-599-272035

Query Match      76.9%; Score 30; DB 15; Length 136;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
DB 24 GVSASSSF 32

RESULT 8
US-10-080-170-155
; Sequence 155, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
```

```
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-080-170-155

Query Match      76.9%; Score 30; DB 14; Length 163;
Best Local Similarity 77.8%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
DB 132 GVAAXSSAF 140

RESULT 9
US-10-080-170-155
; Sequence 155, Application US/10080170
; Publication No. US20040121322A9
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-080-170-155

Query Match      76.9%; Score 30; DB 16; Length 163;
Best Local Similarity 77.8%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
DB 132 GVAAXSSAF 140

RESULT 10
US-10-468-356-155
; Sequence 155, Application US/10468356
; Publication No. US20040197896A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; FILE REFERENCE: 05394.0019
; CURRENT APPLICATION NUMBER: US/10/468,356
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 10/080,170
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 655
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 155
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-468-356-155

Query Match      76.9%; Score 30; DB 17; Length 163;
Best Local Similarity 77.8%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      1  GVNAXSSAF 9
DB      132  GVAASSAF 140

RESULT 11
US-10-080-170-538
; Sequence 538, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; PRIOR FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-538

Query Match      76.9%; Score 30; DB 14; Length 167;
Best Local Similarity 77.8%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GVNAXSSAF 9
DB      136  GVAASSAF 144

RESULT 12
US-10-080-170-538
; Sequence 538, Application US/10080170
; Publication No. US20040121322A9
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-538

Query Match      76.9%; Score 30; DB 16; Length 167;
Best Local Similarity 77.8%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GVNAXSSAF 9
DB      136  GVAASSAF 144

RESULT 13
US-10-468-356-538
; Sequence 538, Application US/10468356
; Publication No. US20040197896A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART

```

```

; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 05394.0019
; CURRENT APPLICATION NUMBER: US/10/468,356
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 10/080,170
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 655
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 538
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-468-356-538

```

```

Query Match      76.9%; Score 30; DB 17; Length 167;
Best Local Similarity 77.8%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1  GVNAXSSAF 9
DB      136  GVAASSAF 144

```

```

RESULT 14
US-10-408-765A-1603
; Sequence 1603, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boi D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary W.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1603
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1603

```

```

Query Match      76.9%; Score 30; DB 16; Length 311;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1  GVNAXSSAF 9
DB      185  GVNASSRF 193

```

```

RESULT 15
US-10-371-525-26
; Sequence 26, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.

```

```
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human lysosomal membrane glycoprotein-1 (LAMP-1)
US-10-371-525-26

Query Match      76.3%; Score 30; DB 14; Length 416;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GVNAXSSAF 9
      |::|||
Db      290 GNVASSSRF 298

Search completed: October 26, 2004, 16:10:14
Job time : 32.5 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:46:55 ; Search time 8.73529 Seconds
(without alignments)
99.132 Million cell updates/sec

Title: US-10-032-950-7

Perfect score: 39

Sequence: 1 GVNAXSSAF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 1008

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	79.5	47	2 C89995	AgrD protein (impo
2	31	79.5	924	2 B95192	hypothetical prote
3	31	79.5	924	2 G98058	hypothetical prote
4	30	76.9	163	2 A87066	conserved hypothet
5	30	76.9	167	2 C70866	hypothetical prote
6	30	76.9	169	2 T45243	hypothetical prote
7	30	76.9	382	2 A28067	lysosomal membrane
8	30	76.9	405	2 A60534	P2B/LAMP-1 precurs
9	30	76.9	407	2 A30200	120K lysosomal mem
10	30	76.9	416	1 A31959	lysosome-associate
11	30	76.9	500	1 E2FF	zip protein precur
12	30	76.9	529	2 T23740	hypothetical prote
13	29	74.4	225	2 T50707	urease accessory p
14	29	74.4	270	1 A38737	gap junction prote
15	29	74.4	270	2 JB0274	connexin 31 - huma
16	29	74.4	270	2 S23590	connexin 31 - mous
17	29	74.4	271	1 B43433	gap junction prote
18	29	74.4	271	1 D42053	gap junction prote
19	29	74.4	316	2 B69315	acetylornithine de
20	29	74.4	333	1 C69812	ferrichrome ABC tr
21	29	74.4	411	2 S75327	lysostaphin - Syne
22	29	74.4	431	2 AD3037	hypothetical prote
23	29	74.4	431	2 G98248	hypothetical prote
24	29	74.4	653	2 T03319	gene 112 protein
25	29	74.4	3635	2 T10053	laminin alpha 5 ch
26	28	71.8	88	2 A82434	conserved hypothet
27	28	71.8	114	2 S50624	hypothetical prote
28	28	71.8	189	2 AC3420	phage minor tail p
29	28	71.8	206	2 A65189	yigW protein - Esc

30 28 71.8 260 2 AF0915 probable deoxyribo
31 28 71.8 260 2 A91225 cytoplasmic Dnase
32 28 71.8 264 2 G86071 hypothetical prote
33 28 71.8 326 2 E86832 oxidoreductase yrb
34 28 71.8 332 2 T04754 hypothetical prote
35 28 71.8 346 2 AC0187 probable iron-side
36 28 71.8 364 2 S43574 COSB5.3 protein (c
37 28 71.8 398 2 F85056 hypothetical prote
38 28 71.8 401 2 C88571 protein COSB5.3 [i
39 28 71.8 453 2 S18597 tubulin beta chain
40 28 71.8 486 2 G96713 probable DNA-bind
41 28 71.8 493 1 S51574 mock protein - Rhi
42 28 71.8 508 2 A32225 nerve growth facto
43 28 71.8 512 2 H76662 probable p1cA prot
44 28 71.8 523 2 G86349 hypothetical prote
45 28 71.8 540 2 S95071 auxin-resistance p

ALIGNMENTS

RESULT 1

C89995 AgrD protein [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: C89995

R:Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiranatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: C89995

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-47 <KUR>

A:Cross-references: UNIPROT:O33586; GB:BA000018; PID:gb13701831; PIDN:BA843124.1; GSPDB:

A:Experimental source: strain N315

C:Genetics:

A:Gene: agrD

Query Match 79.5%; Score 31; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9

Db 24 GVNACSSLF 32

RESULT 2

B95192 hypothetical protein SP1652 [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C:Accession: B95192

R:Petelin, H.; Neilson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radure, D.; Holtzapple,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison

A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: B95192

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-924 <KUR>

A:Cross-references: UNIPROT:Q97FG8; GB:AE005672; PIDN:AAK75731.1; PID:gl4973142; GSPDB:

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP1652

Query Match 79.5%; Score 31; DB 2; Length 924;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
 |:|:|:|:|:
 Db 239 GLNAPSSAY 247

RESULT 3
 G98058
 hypothetical protein spr1496 [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: G98058
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; DeHoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 V, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: G98058
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-924 <KUR>
 A:Cross-references: UNIPROT:Q8CYG6; GB:AB007317; PIDN:AAU00300.1; PID:G15459156; GSPDB:G
 A:Gene: spr1496

Query Match 79.5%; Score 31; DB 2; Length 924;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
 |:|:|:|:|:
 Db 239 GLNAPSSAY 247

RESULT 4
 A87066
 conserved hypothetical protein ML1255 [imported] - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: A87066
 R:Coile, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
 R.; Davies, R.M.; Devlin, K.; Duttoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
 eam, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
 A:Title: Massive gene decay in the leprosy bacillus.
 A:Reference number: A86909; MUID:21128732; PMID:11234002
 A:Accession: A87066
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-163 <STO>
 A:Cross-references: UNIPROT:Q9CC58; GB:AL450380; NID:G13093193; PIDN:CAC31636.1; GSPDB:G
 C:Gene: ML1255
 C:Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16

Query Match 76.9%; Score 30; DB 2; Length 163;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
 |:|:|:|:|:
 Db 132 GVAASAF 140

RESULT 5
 C70866
 hypothetical protein Rv2468c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: C70866
 R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: C70866
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-167 <COL>
 A:Cross-references: UNIPROT:O53195; GB:AL021246; GB:AL123456; NID:G3261507; PIDN:CAA1604
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv2468c
 C:Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16

Query Match 76.9%; Score 30; DB 2; Length 167;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
 |:|:|:|:|:
 Db 136 GVAASAF 144

RESULT 6
 T45243
 hypothetical protein MLCB1610.16 [imported] - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T45243
 R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, March 1999
 A:Reference number: Z22949
 A:Accession: T45243
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-169 <JAM>
 A:Cross-references: UNIPROT:Q9X7B5; EMBL:AL049913; PIDN:CAB43162.1
 A:Experimental source: cosmid B1610
 C:Genetics:
 A:Note: MLCB1610.16
 C:Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16

Query Match 76.9%; Score 30; DB 2; Length 169;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
 |:|:|:|:|:
 Db 138 GVAASAF 146

RESULT 7
 A28067
 lysosomal membrane glycoprotein LAMP-1 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
 C:Accession: A28067
 R:Chen, J.W.; Cha, Y.; Yuku, K.U.; Gracy, R.W.; August, J.T.
 J. Biol. Chem. 263, 8754-8758, 1988
 A:Title: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprote
 A:Reference number: A28067; MUID:88243732; PMID:3379044
 A:Accession: A28067
 A:Molecule type: mRNA
 A:Residues: 1-382 <CHE>
 A:Cross-references: UNIPROT:P11438; GB:J03881; NID:G198706; PIDN:AAA39411.1; PID:G293692
 A:Note: the authors translated the codon ATT for residue 1 as Leu and CCG for residue 2
 C:Superfamily: lysosome-associated membrane protein

C;Keywords: glycoprotein; membrane protein

Query Match 76.9%; Score 30; DB 2; Length 382;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSSAF 9
|:|:|:|:|
Db 256 GVNASSSLF 264

RESULT 8

A60534
P2B/LAMP-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A60534
R;Heffernan, M.; Yousefi, S.; Dennis, J.W.
Cancer Res. 49, 6077-6084, 1989
A;Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastasis
A;Reference number: A60534; MUID:9002989; PMID:2676155
A;Accession: A60534
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-405 <HEF>
A;Cross-references: UNIPROT:P11438
C;Superfamily: lysosome-associated membrane protein

Query Match 76.9%; Score 30; DB 2; Length 405;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSSAF 9
|:|:|:|:|
Db 279 GVNASSSLF 287

RESULT 9

A30200
L20K lysosomal membrane glycoprotein precursor - rat
N;Alternate names: sialoglycoprotein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: A30200; G03331
R;Howe, C.L.; Granger, B.L.; Hull, M.; Green, S.A.; Gabel, C.A.; Helenius, A.; Mellman, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 7577-7581, 1988
A;Title: Derived protein sequence, oligosaccharides, and membrane insertion of the L20-K glycoproteins.
A;Reference number: A30200; MUID:89017240; PMID:3174652
A;Accession: A30200
A;Molecule type: mRNA
A;Residues: 1-407 <HOW>
A;Cross-references: UNIPROT:P14562; EMBL:J03672
R;Himeno, M.; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, K.; Kono, A.; Sakaki, Y.; Kat
FEBS Lett. 244, 351-356, 1989
A;Title: Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in
A;Reference number: S03331; MUID:89153580; PMID:2920835
A;Accession: S03331
A;Molecule type: mRNA
A;Residues: 22-407 <HIM>
A;Cross-references: EMBL:X14765; NID:G56577; PIDN:CAA32873.1; PID:G56578
A;Note: the authors translated the codon GGG for residue 15 as Val
C;Superfamily: lysosome-associated membrane protein
C;Keywords: glycoprotein; membrane protein
P;22-407/Product: lysosomal membrane glycoprotein, 107K #status experimental <MAT>

Query Match 76.9%; Score 30; DB 2; Length 407;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSSAF 9
|:|:|:|:|

Db 281 GVNATSSSLF 289

RESULT 10

A31959
lysosome-associated membrane protein 1 precursor - human
N;Alternate names: lysosomal-associated membrane protein lamp A; major lysosomal membra
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: A31959; B46044; S02150; A23656; A32685; S34737; A30210; B30210
R;Fukuda, M.; Viitala, J.; Matteson, J.; Carlsson, S.R.
J. Biol. Chem. 263, 18920-18928, 1988
A;Title: Cloning of cDNAs encoding human lysosomal membrane glycoproteins, h-lamp-1 and
A;Reference number: A32699; MUID:89066687; PMID:3198605
A;Accession: A31959
A;Molecule type: mRNA
A;Residues: 1-416 <FUK>
A;Cross-references: UNIPROT:P11279; GB:J04182; NID:gl86927; PIDN:AAA60382.1; PID:G30710
R;Sawada, R.; Jardine, K.A.; Fukuda, M.
J. Biol. Chem. 268, 9014-9022, 1993
A;Title: The genes of major lysosomal membrane glycoproteins, lamp-1 and lamp-2. 5'-fla
A;Reference number: A46044; MUID:93232065; PMID:8517882
A;Accession: B46044
A;Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tr.
A;Molecule type: DNA
A;Residues: 1-416 <SAW>
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBI:P:129878)
R;Mane, S.M.; Marzella, L.; Bainton, D.F.; Holt, V.K.; Cha, Y.; Hildreth, J.E.K.; Augus
Arch. Biochem. Biophys. 268, 360-378, 1989
A;Title: Purification and characterization of human lysosomal membrane glycoproteins.
A;Reference number: S02150; MUID:89104438; PMID:2912382
A;Accession: S02150
A;Molecule type: protein
A;Residues: 28-35; 'X', 37-39; 'X', 41-43; 'X', 45-58 <MAN>
R;Carlsson, S.R.; Fukuda, M.
J. Biol. Chem. 265, 20488-20495, 1990
A;Title: The polylactosaminoglycans of human lysosomal membrane glycoproteins lamp-1 an
A;Reference number: A32656; MUID:91056099; PMID:2243102
A;Accession: A32656
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 57-71; 116-135; 215-234 <CAR>
R;Carlsson, S.R.; Fukuda, M.
J. Biol. Chem. 264, 20526-20531, 1989
A;Title: Structure of human lysosomal membrane glycoprotein 1. Assignment of disulfide
A;Reference number: A32685; MUID:90062189; PMID:2584229
A;Accession: A32685
A;Molecule type: protein
A;Residues: 31-35; 72-74; 'X', 76-77; 144-153; 177-179; 'X', 181-187; 215-219; 255-259; 'X', 261-2
R;Carlsson, S.R.; Lyckseil, P.O.; Fukuda, M.
Arch. Biochem. Biophys. 304, 65-73, 1993
A;Title: Assignment of O-glycan attachment sites to the hinge-like regions of human lys
A;Reference number: S34737; MUID:93312023; PMID:8323299
A;Accession: S34737
A;Molecule type: protein
A;Residues: 190-214 <CA3>
R;Viitala, J.; Carlsson, S.R.; Siebert, P.D.; Fukuda, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 3743-3747, 1988
A;Title: Molecular cloning of cDNAs encoding lamp A, a human lysosomal membrane glycopr
A;Reference number: A30210; MUID:88234502; PMID:3131762
A;Accession: A30210
A;Molecule type: mRNA
A;Residues: 'MARGGVR', 40-416 <VII>
A;Cross-references: GB:J03263; NID:gl87178; PIDN:AAA59524.1; PID:G307132
A;Molecule type: protein
A;Residues: 116-119; 'X', 121-128; 'X', 130-131; 'X', 133-135; 163; 'X', 165-179; 'X', 181-189; 'X',
C;Genetics:
A;Gene: GDB:ILAMP1
A;Cross-references: GDB:120137; OMIM:153330
A;Map position: 13q34-13q34
C;Superfamily: lysosome-associated membrane protein

C;Keywords: glycoprotein; lysosome; transmembrane protein
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-416/Product: lysosomal membrane glycoprotein 1 #status predicted <MAT>
F;28-381/Domain: lysosomal luminal #status predicted <LYS>
F;382-405/Domain: transmembrane #status predicted <TM>
F;406-416/Domain: intracellular #status predicted <CYT>
F;36-44,83,102,106,240,248,292,322,379/Binding site: carbohydrate (Asn) (covalent) #stat
F;40-79,154-190,230-268,331-374/Disulfide bonds: #status experimental
F;61,75,120,129,164,180,222,227,260/Binding site: carbohydrate (Asn) (covalent) #status
F;136/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F;138,199/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;206,208,210/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 76.9%; Score 30; DB 1; Length 416;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
|:|:|:|:|
Db 290 GVNASSRF 298

RESULT 11
EPFF
zip protein precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: zipper protein
C;Species: Drosophila melanogaster
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: S00483; A37532
R;Zhao, D.B.; Cote, S.; Jaehnig, F.; Haller, J.; Jaecle, H.
EMBO J. 7, 1115-1119, 1988
A;Title: Zipper encodes a putative integral membrane protein required for normal axon pa
A;Reference number: S00483; MUID:88296414; PMID:3402433
A;Accession: S00483
A;Molecule type: DNA
A;Residues: 1-500 <ZHA>
A;Cross-references: UNIPROT:P10379; GB:X07450; NID:g8854; PIDN:CAA30332.1; PID:g8855
A;Accession: A37532
A;Molecule type: mRNA
A;Residues: 1-500 <ZHA1>
A;Cross-references: EMBL:X07450; NID:g8854; PIDN:CAA30332.1; PID:g8855
C;Genetics:
A;Gene: zip
A;Cross-references: FlyBase:FBgn0004055
A;Introns: 237/1; 354/1
C;Superfamily: zip protein
C;Keywords: glycoprotein; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-500/Product: zip protein #status predicted <MAT>
F;22-470/Domain: extracellular #status predicted <EXT>
F;466-486/Domain: transmembrane #status predicted <TM>
F;496-500/Domain: intracellular #status predicted <INT>
F;35,233,317,374,448/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.9%; Score 30; DB 1; Length 500;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 1 GVNAXSSAF 9
|:|:|:|:|
Db 463 GVNAGSTF 471

RESULT 12
T23740
hypothetical protein M106.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23740
R;Palmer, S.
submitted to the EMBL Data Library, December 1994
A;Reference number: 219792
A;Accession: T23740

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-529 <WIL>
A;Cross-references: UNIPROT:Q09593; EMBL:Z46935; PIDN:CAA87050.1; GSPDB:GNC0020; CESP:ML
A;Experimental source: clone M106
C;Genetics:
A;Gene: CESP:M106.3
A;Map position: 2
A;Introns: 34/1; 175/3; 224/3; 271/3; 341/3; 372/1; 401/3; 446/3; 475/3; 494/3
Query Match 76.9%; Score 30; DB 2; Length 529;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
|:|:|:|:|
Db 349 GVNAPSAP 357

RESULT 13
T50707
urease accessory protein D [imported] - Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50707
R;Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2
A;Reference number: 225222; MUID:20115911; PMID:10648776
A;Accession: T50707
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-225 <CHO>
A;Cross-references: UNIPROT:Q9RFF6; EMBL:AF195122; PIDN:AAF24251.1
A;Experimental source: strain 2.4.1
C;Genetics:
C;Superfamily: urease accessory protein UreH/UreD

Query Match 74.4%; Score 29; DB 2; Length 225;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
|:|:|:|:|
Db 179 GVEAASAF 187

RESULT 14
A38737
Gap junction protein Cx31 - rat
N;Alternate names: connexin-31
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Sep-1991 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
C;Accession: A38737
R;Hoh, J.H.; John, S.A.; Revel, J.P.
J. Biol. Chem. 266, 6524-6531, 1991
A;Title: Molecular cloning and characterization of a new member of the gap junction gene
A;Reference number: A38737; MUID:91177912; PMID:1706719
A;Molecule type: DNA
A;Accession: A38737
A;Residues: 1-270 <HOH>
A;Cross-references: UNIPROT:P25305; GB:M59936; NID:g203659; PIDN:AAA40997.1; PID:g203660
A;Note: the authors translated the codon CAG for residue 7 as Gly and GAC for residue 8
C;Superfamily: gap junction protein
C;Keywords: gap junction; phosphoprotein; placenta; transmembrane protein
F;1-20/Domain: intracellular #status predicted <INT1>
F;21-40/Domain: transmembrane #status predicted <TM1>
F;41-73/Domain: extracellular #status predicted <E1>
F;74-96/Domain: transmembrane #status predicted <TM2>
F;97-122/Domain: intracellular #status predicted <INT2>
F;123-159/Domain: transmembrane #status predicted <TM3>
F;160-184/Domain: extracellular #status predicted <E2>

F:185-207/Domain: transmembrane #status predicted <TM4>
 F:208-270/Domain: intracellular #status predicted <INT3>

Query Match 74.4%; Score 29; DB 1; Length 270;
 Best Local Similarity 66.7%; Pred. No. 38;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Caps 0;

QY 1 GVNAXSSAF 9
 |||||
 Db 12 GVNQYSTAF 20

RESULT 15

JE0274
 connexin 31 - human
 N:Alternate names: gap junction protein beta 3, 31X
 C:Species: Homo sapiens (man)
 C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
 C:Accession: JE0274
 R:Wenzel, K.; Manthey, D.; Willecke, K.; Grzeschik, K.H.; Traub, O.
 Biochem. Biophys. Res. Commun. 248, 910-915, 1998
 A:Title: Human gap junction protein connexin31: Molecular cloning and expression analysis
 A:Reference number: JE0274; MUID:98369649; PMID:9704026
 A:Accession: JE0274
 A:Molecule type: mRNA
 A:Residues: 1-270 <WEN>
 A:Cross-references: UNIPROT:O75712; GB:AJ004856; NID:g3445286; PIDN:CAA06165.1; PID:g344
 C:Genetics:
 A:Gene: GDB:GJB3
 A:Cross-references: GDB:127820
 A:Map position: lp34-lp36
 C:Superfamily: gap junction protein

Query Match 74.4%; Score 29; DB 2; Length 270;
 Best Local Similarity 66.7%; Pred. No. 38;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Caps 0;

QY 1 GVNAXSSAF 9
 |||||
 Db 12 GVNKYSTAF 20

Search completed: October 26, 2004, 16:06:11
 Job time : 9.73529 secs

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:50 ; Search time 40.6324 Seconds
(without alignments)
127.445 Million cell updates/sec

Title: US-10-032-950-7

Perfect score: 39

Sequence: 1 GVNAXSSAF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	87.2	303	2 Q6NC24	Q6nc24 rhodopsu
2	34	87.2	303	2 CAE26093	Ca26093 rhodopsu
3	32	82.1	236	2 Q9X494	Q9x494 mycoplasma
4	32	82.1	745	2 Q74F43	Q74f43 geobacter s
5	32	82.1	745	2 AAR34096	Aar34096 geobacter
6	31	79.5	47	2 Q33586	Q33586 staphylococ
7	31	79.5	47	2 Q7A2N4	Q7a2n4 staphylococ
8	31	79.5	47	2 Q7A417	Q7a417 staphylococ
9	31	79.5	47	2 CAE92745	Ca26093 rhodopsu
10	31	79.5	47	2 CAE92748	Ca26093 rhodopsu
11	31	79.5	47	2 CAE92751	Ca26093 rhodopsu
12	31	79.5	47	2 CAE92754	Ca26093 rhodopsu
13	31	79.5	47	2 CAE92757	Ca26093 rhodopsu
14	31	79.5	543	2 Q7X3X6	Q7x3x6 clavibacter
15	31	79.5	924	2 Q8CYG6	Q8cyg6 streptococ
16	31	79.5	924	2 Q97PQ8	Q97p8 streptococ
17	31	79.5	959	2 Q6C733	Q6c733 yarrowia li
18	31	79.5	1203	2 Q7PSN7	Q7psn7 anopheles g
19	30	76.9	115	2 Q88TX8	Q88tx8 lactobacilli
20	30	76.9	158	2 Q73XN1	Q73xn1 mycobacteri
21	30	76.9	158	2 AAS04605	Aas04605 mycobacte
22	30	76.9	163	2 Q9CC58	Q9cc58 mycobacteri
23	30	76.9	167	2 Q53195	Q53195 mycobacteri
24	30	76.9	167	2 Q7TVI6	Q7tvi6 mycobacteri
25	30	76.9	169	2 Q9X7B5	Q9x7b5 mycobacteri
26	30	76.9	189	2 Q922T9	Q922t9 mus musculu
27	30	76.9	214	2 Q8M6L3	Q8m6l3 taenia soli
28	30	76.9	248	2 Q96140	Q96140 homo sapien
29	30	76.9	278	2 Q7QVJ5	Q7qvj5 giardia lam
30	30	76.9	308	2 Q9BRD2	Q9brd2 homo sapien
31	30	76.9	355	2 Q9NPL3	Q9npl3 homo sapien

32 30 76.9 406 1 LMPI_MOUSE
33 30 76.9 406 2 Q8VH34
34 30 76.9 407 1 LMPI_RAT
35 30 76.9 407 2 Q9DCI3
36 30 76.9 416 1 LMPI_HUMAN
37 30 76.9 417 2 Q8WDU3
38 30 76.9 469 2 Q6NBU0
39 30 76.9 469 2 CAE26182
40 30 76.9 488 1 UZIP_DROME
41 30 76.9 529 2 Q09593
42 30 76.9 610 2 Q6FU80
43 30 76.9 655 2 Q8IRV2
44 30 76.9 659 2 Q8MT98
45 30 76.9 809 2 O76869

ALIGNMENTS

RESULT 1

Q6NC24 PRELIMINARY; PRT; 303 AA.
ID Q6NC24;
AC Q6NC24;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Possible flagellin and hook associated protein.
DE Name=flgI; OrderedLocustNames=RPA0649;
OS Rhodopsseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopsseudomonas.
OX NCBI_TaxID=1076;
RN [1]_TaxID=1076;
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L., Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres J.L., Perez C., Harrison F.H., Gibson J., Harwood C.S.;
RA "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopsseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
KW Complete proteome; Flagellum.
SQ SEQUENCE 303 AA; 31313 MW; 3243B8F1F30D2CB7 CRC64;

Query Match 87.2%; Score 34; DB 2; Length 303;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9

DB 186 GVNADNSAF 194

RESULT 2

CAE26093 PRELIMINARY; PRT; 303 AA.
ID CAE26093
AC CAE26093;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE Possible flagellin and hook associated protein.
DE FLGL OR RPA0649.
OS Rhodopsseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopsseudomonas.
OX NCBI_TaxID=1076;
RN [1]_TaxID=1076;
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707;

RA Laximer F.W., Chain P., Hauser L., Lamerdin J., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Petes C.,
RA Harrison F.H., Gibson J., Harwood C.S.,
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodospirillum rubrum palustris."
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX2595; CA26093.1; -
SQ SEQUENCE 303 AA; 31313 MW; 3243B8F1F30D2CB7 CRC64;

Query Match 87.2%; Score 34; DB 2; Length 303;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSAF 9
Db 186 GVNADNSAF 194

RESULT 3
ID Q9X494 PRELIMINARY; PRT; 236 AA.
AC Q9X494;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Yabc protein.
GN Name=Yabc;
OS Mycoplasma fermentans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2115;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG18;
RX MEDLINE=99115554; PubMed=9916088;
RA Calcutt M.J., Kim M.F., Karpas A.B., Muhlrad P.F., Wise K.S.;
RT "Differential posttranslational processing confers intraspecies
RT variation of a major surface lipoprotein and a macrophage-activating
RL lipopeptide of Mycoplasma fermentans."
RL Infect. Immun. 67:760-771(1999).
DR EMBL; AF100324; AAD25734.1; -
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000878; Cor/por Mettransf.
DR InterPro; IPR008189; UPF011-
DR Pfam; PF00590; TP_methylase; 1.
DR TIGRFAMs; TIGR00096; UPF0011; 1.
DR PROSITE; PS01296; UPF0011; 1.
SQ SEQUENCE 236 AA; 26620 MW; F12974232C6E0A35 CRC64;

Query Match 82.1%; Score 32; DB 2; Length 236;
Best Local Similarity 77.8%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSAF 9
Db 112 GVNAAISAF 120

RESULT 4
ID Q74F43 PRELIMINARY; PRT; 745 AA.
AC Q74F43;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Methyl-accepting chemotaxis protein, putative.
GN ORFNames=GSU0766;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OX Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.J., Khouri H.M., Feldblyum T.V., Uterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.W.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments."
RL Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR34096.1; -
DR TIGR; GSU0766; -
DR InterPro; IPR004089; Chmtaxis_trans.
DR InterPro; IPR003660; HAMP.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; MA; 1.
DR PROSITE; PS01111; CHEMOTAXIS_TRANSLOC_2; 1.
DR PROSITE; PS00885; HAMP; 1.
SQ SEQUENCE 745 AA; 79920 MW; E61D6ED81FC095C3 CRC64;

Query Match 82.1%; Score 32; DB 2; Length 745;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSSA 8
Db 326 GVNAASSA 333

RESULT 5
ID AAR34096 PRELIMINARY; PRT; 745 AA.
AC AAR34096;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Methyl-accepting chemotaxis protein, putative.
GN GSU0766.
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OX Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.J., Khouri H.M., Feldblyum T.V., Uterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.W.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments."
RL Science 302:1967-1969(2003).
DR EMBL; AE017209; AAR34096.1; -
DR TIGR; GSU0766; -
SQ SEQUENCE 745 AA; 79920 MW; E61D6ED81FC095C3 CRC64;

Query Match 82.1%; Score 32; DB 2; Length 745;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVNAXSSA 8
Db 326 GVNAASSA 333

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RESULT 6
O33586      PRELIMINARY;      PRT;      47 AA.
AC O33586;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE AgRD.
GN Name=agrD;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=SA502A;
RX MEDLINE=97342847; PubMed=9197262;
RA Ji G., Beavis R., Novick R.P.;
RT "Bacterial interference caused by autoinducing peptide variants.";
RL Science 276:2027-2030(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Gt31a-cp5, Gt31b-cp5, Gt36a-cp8, Gt36b-cp8, and Gt111-cp8;
RA Goerke C., Dabach S., Kuemmel M., Wolz C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001782; AAB63265.1; -
DR EMBL; AJ617715; CA92745.1; -
DR EMBL; AJ617716; CA92748.1; -
DR EMBL; AJ617717; CA92751.1; -
DR EMBL; AJ617718; CA92754.1; -
DR EMBL; AJ617719; CA92757.1; -
DR PIR; C89995; C89995.
DR InterPro; IPR009229; AgRD.
DR Pfam; PF05931; AgRD; 1.
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 79.5%; Score 31; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
DB 24 GVNACSLF 32

RESULT 7
O7A2N4      PRELIMINARY;      PRT;      47 AA.
AC O7A2N4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AgRD protein.
GN Name=agrD; OrderedLocusNames=SAV2037;
OS Staphylococcus aureus (strain Mx50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RC SEQUENCE FROM N.A.
RP MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003364; BAB58199.1; -
DR InterPro; IPR009229; AgRD.
DR Pfam; PF05931; AgRD; 1.
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 79.5%; Score 31; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
DB 24 GVNACSLF 32

RESULT 8
O7A4I7      PRELIMINARY;      PRT;      47 AA.
AC O7A4I7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AgRD protein.
GN Name=agrD; OrderedLocusNames=SA1842.1; ORFNames=SA5066;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RC SEQUENCE FROM N.A.
RP MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003364; BAB58199.1; -
DR InterPro; IPR009229; AgRD.
DR Pfam; PF05931; AgRD; 1.
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match 79.5%; Score 31; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVNAXSSAF 9
DB 24 GVNACSLF 32

RESULT 9
CAE92745    PRELIMINARY;      PRT;      47 AA.
AC CAE92745;
DT 01-APR-2004 (TrEMBLrel. 27, Created)
DT 01-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE AgRD protein.
GN AgRD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RC STRAIN=gt31a-cp5;
RP SEQUENCE FROM N.A.
RA Goerke C., Dabach S., Kuemmel M., Wolz C.;
RT "Evolutionary Models for the development of the Polymorphic Loci agr
RT and cap in Staphylococcus aureus.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ617715; CA92745.1; -
DR Pfam; PF05931; AgRD; 1.
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

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Query Match      79.5%; Score 31; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSSAF 9
    |||||
Db 24 GVNACSSLF 32

RESULT 10
CAE92748 PRELIMINARY; PRT; 47 AA.
AC CAE92748;
DT 01-APR-2004 (TRENBLrel. 27, Created)
DT 01-APR-2004 (TRENBLrel. 27, Last sequence update)
DT 01-APR-2004 (TRENBLrel. 27, Last annotation update)
DE AGD protein.
GN AGRD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=gt31b-cp5;
RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
RT "Evolutionary Models for the Development of the Polymorphic Loci agr
and cap in Staphylococcus aureus.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ617716; CAE92748.1; -
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match      79.5%; Score 31; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSSAF 9
    |||||
Db 24 GVNACSSLF 32

RESULT 11
CAE92751 PRELIMINARY; PRT; 47 AA.
AC CAE92751;
DT 01-APR-2004 (TRENBLrel. 27, Created)
DT 01-APR-2004 (TRENBLrel. 27, Last sequence update)
DT 01-APR-2004 (TRENBLrel. 27, Last annotation update)
DE AGD protein.
GN AGRD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=gt36a-cp8;
RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
RT "Evolutionary Models for the Development of the Polymorphic Loci agr
and cap in Staphylococcus aureus.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ617717; CAE92751.1; -
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match      79.5%; Score 31; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSSAF 9
    |||||
Db 24 GVNACSSLF 32

RESULT 12
CAE92754 PRELIMINARY; PRT; 47 AA.
AC CAE92754;
DT 01-APR-2004 (TRENBLrel. 27, Created)
DT 01-APR-2004 (TRENBLrel. 27, Last sequence update)
DT 01-APR-2004 (TRENBLrel. 27, Last annotation update)
DE AGD protein.
GN AGRD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=gt36b-cp8;
RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
RT "Evolutionary Models for the Development of the Polymorphic Loci agr
and cap in Staphylococcus aureus.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ617718; CAE92754.1; -
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match      79.5%; Score 31; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSSAF 9
    |||||
Db 24 GVNACSSLF 32

RESULT 13
CAE92757 PRELIMINARY; PRT; 47 AA.
AC CAE92757;
DT 01-APR-2004 (TRENBLrel. 27, Created)
DT 01-APR-2004 (TRENBLrel. 27, Last sequence update)
DT 01-APR-2004 (TRENBLrel. 27, Last annotation update)
DE AGD protein.
GN AGRD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=gt111-cp8;
RA Goerke C., Dasbach S., Kuemmel M., Wolz C.;
RT "Evolutionary Models for the Development of the Polymorphic Loci agr
and cap in Staphylococcus aureus.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ617719; CAE92757.1; -
SQ SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;

Query Match      79.5%; Score 31; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVNAXSSAF 9
    |||||
Db 24 GVNACSSLF 32

RESULT 14
QX3X6 PRELIMINARY; PRT; 543 AA.
AC QX3X6;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative tomatinase TomA.
GN Name=toma;
OS Clavibacter michiganensis subsp. michiganensis.
OC Bacteria; Actinobacteria; Actinobacteriales; Clavibacter.
OC Micrococccineae; Microbacteriaceae; Clavibacter.

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OX  NCBI_TaxID=33013;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=NCPPB362;
RA  Gartenmann K.-H., Graefen I., Zellermann E.-M., Burger A.,
RA  Eichenlaub R.;
RL  Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AF393183; AAS7293.1; -
DR  GO: 0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR  GO: 0005975; P:carbohydrate metabolism; IEA.
DR  InterPro: IPR01000; Glyco_hydro_10.
DR  Pfam: PF00331; Glyco_hydro_10; 1.
DR  SMART: SM00633; Glyco_10; 1.
SQ  SEQUENCE 543 AA; 58175 MW; 8ECC284F8A521AED CRC64;

Query Match      79.5%; Score 31; DB 2; Length 924;
Best Local Similarity 66.7%; Pred.No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 GVNAXSSAF 9
Db  478 GINATSYAF 486

RESULT 15
Q8CYG6
AC  Q8CYG6      PRELIMINARY;      PRT;      924 AA.
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Hypothetical protein spr1496.
GN  OrderedLocusNames=spr1496;
OS  Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC  Streptococcus.
OX  NCBI_TaxID=171101;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21429245; PubMed=11544234;
RA  Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA  DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA  Gilmour R., Glass J.S., Khoja H., Kraft A.R., Legace R.E.,
RA  LeBlanc D.J., Lee L.N., Leikowitz E.J., Lu J., Matsushima P.,
RA  McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
RA  Norris F.H., O'Garra M., Peery R.B., Robertson G.T., Rockey P.,
RA  Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA  Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,
RA  Glass J.L.;
RT  "genome of the bacterium Streptococcus pneumoniae strain R6.";
RL  J. Bacteriol. 183:5709-5717(2001).
DR  EMBL: AE008518; AAL00300.1; -.
DR  PIR: G98058; G98058.
DR  GO: 0016020; C:membrane; IEA.
DR  InterPro: IPR003838; DUF214.
DR  Pfam: PF02687; PfsX; 2.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 924 AA; 102967 MW; 192383CF91548592 CRC64;

Query Match      79.5%; Score 31; DB 2; Length 924;
Best Local Similarity 66.7%; Pred.No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  1 GVNAXSSAF 9
Db  239 GLNAFSSAF 247

Search completed: October 26, 2004, 16:05:07
Job time : 42.6324 secs

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:15 ; Search time 23.75 Seconds
(without alignments)
75.522 Million cell updates/sec

Title: US-10-032-950-8

Perfect score: 19

Sequence: 1 XSLIF 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	94.7	4	2 AAY16582	Aay16582 Antibacte
2	18	94.7	5	3 AAY67858	Aay67858 S. aureus
3	18	94.7	5	5 AAM50906	Aam50906 AgrD-auto
4	18	94.7	5	5 ABP53547	Abp53547 Cyclic pe
5	18	94.7	5	7 ADD11974	Add11974 Cell adhe
6	18	94.7	6	2 AAR10519	Aar10519 Fusinus i
7	18	94.7	6	2 AAW25555	Aaw25555 Synthetic
8	18	94.7	6	2 AAW10783	Aaw10783 Ferritin
9	18	94.7	6	2 AAW25549	Aaw25549 Synthetic
10	18	94.7	6	2 AAW25550	Aaw25550 Synthetic
11	18	94.7	6	7 ADD11975	Add11975 Cell adhe
12	18	94.7	7	2 AAW10802	Aaw10802 Ferritin
13	18	94.7	7	2 AAW10801	Aaw10801 Ferritin
14	18	94.7	7	2 AAW10784	Aaw10784 Ferritin
15	18	94.7	7	2 AAW10779	Aaw10779 Ferritin
16	18	94.7	7	2 AAW10778	Aaw10778 Ferritin
17	18	94.7	7	5 ABG96785	Abg96785 Human leu
18	18	94.7	7	7 ADD11976	Add11976 Cell adhe
19	18	94.7	7	7 ADL98602	Adl98602 Human leu
20	18	94.7	8	2 AAW25556	Aaw25556 Synthetic
21	18	94.7	8	5 AAU63684	Aau63684 Cell deat
22	18	94.7	8	7 ADD11977	Add11977 Cell adhe
23	18	94.7	9	2 AAW38323	Aaw38323 Transcrip
24	18	94.7	9	3 AAY67854	Aay67854 S. aureus
25	18	94.7	9	3 AAY67860	Aay67860 Staphyloc

ALIGNMENTS

RESULT 1.

AAY16582

ID AAY16582 standard; peptide; 4 AA.

XX AC AAY16582;

XX DT 13-AUG-1999 (first entry)

XX DE Antibacterial cyclic oligopeptide for Staphylococcus strains.

XX KW Cyclic peptide; modulator; agr response; virulence;

XX KW cell wall protein production; prophylaxis; exotoxin secretion;

XX KW bacterial infection; toxic shock syndrome; Staphylococci;

XX KW Staphylococcus aureus; coagulase-negative S. epidermidis;

XX KW medical implant infection; cyclic.

XX OS Synthetic.

XX Key

FT Misc-difference 1. .4

FT /note= "linked by -O-CH(NHX)-(CH2)n-S, where X is

FT comprises 2-5 amino acids, and is not Gly-Val-Asn-Ala

FT (claim 1) or is Gly-Val-Asn-Ala (claim 8)"

FT Location/Qualifiers

XX MO9926968-A1.

XX 03-JUN-1999.

XX 24-NOV-1998; 98WO-GB003497.

XX 26-NOV-1997; 97GB-00024859.

XX (UYN0-) UNIV NOTTINGHAM.

XX Bycroft BW, Williams P, Stewart GSAB, Chan WC, McDowell PW;

XX Affas ZM;

XX WPI; 1999-370885/31.

XX Cyclic antibacterial peptides for treating and preventing bacterial

XX infection in humans and animals.

XX Claim 1; Page; 32pp; English.

XX The present sequence represents a cyclic peptide which is a modulator of
CC the agr response. Agonists of this response antagonize early stages of
CC virulence, specifically production of cell wall proteins (so are
CC preferred for prophylaxis), while antagonists interfere with the later

CC stages of virulence, specifically secretion of exotoxin (so are preferred
 CC for treatment). The peptides are used to treat or prevent bacterial
 CC infections in humans and animals, also for incorporation into medical
 CC articles, e.g. tampons (to prevent toxic shock syndrome), prostheses and
 CC wound dressings. Particularly they are active against staphylococci,
 CC specifically staphylococcus aureus but also coagulase-negative S.
 CC epidermidis, implicated in infection of medical implants. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX Sequence 4 AA;

Query Match 94.7%; Score 18; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSFLF 5
 DB 1 SSFLF 4

RESULT 2

ID AAY67858 standard; peptide; 5 AA.

XX AAY67858;

DT 25-APR-2000 (first entry)

DE S. aureus peptide #8 used for bacterial interference.

XX Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;
 KW virulence factor; treatment.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Misc-difference 1

FT /label= Unknown
 FT /note= "N-terminal residue is linked to the C-terminal
 FT residue to form a cyclic peptide"

PN WO9967286-A2.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-US014562.

XX 24-JUN-1998; 98US-00103438.

XX (UVRQ) UNIV ROCKEFELLER.

XX (UUNY) UNIV NEW YORK STATE.

XX Muir TW, Mayville P, Novick RP, Ji G, Beavis R;

XX WPI; 2000-147202/13.

XX New cyclic peptides for treating infections with Staphylococcus aureus.

XX Claim 9; Page 26; 37pp; English.

XX This sequence represents a cyclic peptide derived from the Staphylococcus
 CC aureus AgrD peptide. The invention relates to AgrD derived peptides, a
 CC composition containing a peptide and a carrier, and a method for the
 CC production of the cyclic peptides. The peptide inhibits the agr response,
 CC which is normally associated with the release of virulence factors of
 CC Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
 CC activates the agr response in strains of a single group, but interferes
 CC with this response in strains of different groups. The peptides and
 CC composition containing them can be used to treat infections by S. aureus

XX Sequence 5 AA;

Query Match 94.7%; Score 18; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSFLF 5
 DB 2 SSFLF 5

RESULT 3

ID AAM50906 standard; peptide; 5 AA.

XX AAM50906;

DT 08-MAY-2002 (first entry)

DE AgrD-autoinducing cyclic peptide, inhibitor of agr response.

XX Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic;
 KW antibacterial; infection; therapy; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "note linked to residue 5 to form cyclic peptide"

FT Misc-difference 1 /note= "any amino acid"

FT Misc-difference 5 /note= "note linked to residue 1 to form cyclic peptide"

XX US6337385-B1.

XX 08-JAN-2002.

XX 24-JUN-1999; 99US-00339511.

XX 24-JUN-1998; 98US-0090402P.

XX (UVRQ) UNIV ROCKEFELLER.

XX (UUNY) UNIV NEW YORK STATE.

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX WPI; 2002-170774/22.

XX Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial
 PT interference and for treating Staphylococcus aureus infection in a
 PT subject.

XX Claim 7; Col 19; 18pp; English.

XX The present sequence is that of a novel synthetic cyclic peptide of the
 CC invention that is capable of inhibiting the agr response of
 CC Staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is
 CC a secreted agr-encoded peptide and where the agr locus controls the
 CC synthesis of virulence factor and other extracellular proteins
 CC responsible for pathogenicity in S. aureus. Preferred peptides may have
 CC the sequence NH₂-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z
 CC residue and COOH other than a thioester bond, where X is an amino acid,
 CC an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a
 CC synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The
 CC cyclic bond is especially a lactam or lactone bond. The thiolactone
 CC structure within native AgrD peptides is required for activation of the
 CC agr response. Elimination of the thiol ester component of the cyclic ring
 CC structure can destroy agr response activating activity while preserving
 CC and enhancing inhibitory activity. A claimed method of preparing a cyclic
 CC peptide involves: assembling a linear peptide chain on to a solid phase
 CC resin support; deprotecting the resulting protected assembled peptide;
 CC treating the deprotected peptide with neutral buffer for a time
 CC sufficient to form the cyclic peptide and cleave the peptide from the
 CC support; and recovering the cyclic peptide. The peptide is useful for

CC bacterial interference, especially for the treatment of *S. aureus*
 CC infection

SQ Sequence 5 AA;

Query Match 94.7%; Score 18; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSIF 5
 DB ||||
 2 SSIF 5

RESULT 4

ABP53547
 ID ABP53547 standard; peptide; 5 AA.

XX AC

XX AC

XX DT

XX 13-DEC-2002 (first entry)

XX DE

XX Cyclic peptide SEQ ID NO:8.

XX KW

XX Cyclic peptide; *Staphylococcus aureus*; infection; antibacterial;
 agr response inhibitor.

XX OS

XX Synthetic.

XX FH

XX Key Location/Qualifiers

FT Misc-difference 1

FT /note= "any amino acid"

PN US2002077453-A1.

XX 20-JUN-2002.

XX 27-DEC-2001; 2001US-00032950.

XX 24-JUN-1998; 98US-0090402P.

XX 24-JUN-1999; 99US-00339511.

XX (MUIR/) MUIR T W.

XX (MAYV/) MAYVILLE P.

XX (NOVI/) NOVICK R P.

XX (BEAV/) BEAVIS R.

XX (JIGG/) JI G.

XX Muir TW, Mayville P, Novick RP, Beavis R, Ji G;

XX WPI; 2002-681366/73.

XX New cyclic peptides, useful for treating *Staphylococcus aureus*

XX infections.

XX Claim 9; Page 10; 18pp; English.

XX ABP53540 to ABP53547 represent cyclic peptides (I) from the present

XX invention. The present invention also describes a method for treating

XX *Staphylococcus aureus* infection comprising the administration of a

XX composition comprising (I). (I) has antibacterial activity, and can be

XX used as an agr gene response inhibitor. The peptides are useful for

XX treating *S. aureus* infections

XX SQ Sequence 5 AA;

Query Match 94.7%; Score 18; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSIF 5

DB ||||

2 SSIF 5

RESULT 5

ADD11974

XX ID

XX ADD11974 standard; peptide; 5 AA.

XX AC

XX ADD11974;

XX DT

XX 01-JAN-2004 (first entry)

XX XX

XX DE

XX Cell adhesion molecule PL protein C-terminal core peptide #277.

XX KW

XX modulator; PDZ; post-synaptic density protein 95; PSD95;

XX Drosophila large disc protein; Zonula Occludin 1 protein; ZO-1;

XX PDZ ligand; PL; anti-inflammatory; anti-allergic; anti-cancer; antipsoriatic;

XX antiasthmatic; dermatological; neuroprotective; virucide; antidiabetic;

XX osteoarthritic; immunosuppressive; antiatherosclerotic;

XX cytostatic; anti-HIV; vasotropic; immunomodulator; neurological disease;

XX immune response disease; muscular disease; cancer;

XX modulating vesicular trafficking; tumour suppression;

XX signal transduction; protein sorting; membrane polarity; apoptosis;

XX synapse formation; multi-protein complex; leukocyte activation inhibitor;

XX cell adhesion molecule.

XX Unidentified.

XX OS

XX WO2003014303-A2.

XX PN

XX 20-FEB-2003.

XX PD

XX 02-AUG-2002; 2002WO-US024655.

XX PF

XX 03-AUG-2001; 2001US-0309841P.

XX PR

XX 25-FEB-2002; 2002US-0360061P.

XX PA

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS,

XX Rabinowitz JD, Schweizer J, Carrick DM;

XX WPI; 2003-368193/26.

XX Modulator of binding between discs-large homology repeat protein, PDZ and

XX PDZ ligand protein, is a peptide having few residues of C-terminal

XX sequence of PDZ ligand protein.

XX Disclosure; Page 35; 172pp; English.

XX The invention relates to a novel modulator of binding between a PDZ

XX protein (post-synaptic density protein 95 (PSD95), Drosophila large disc

XX protein and Zonula Occludin 1 protein (ZO-1)) and a PDZ ligand (PL)

XX protein. The modulator is a peptide having 3 residues of a C-terminal

XX sequence of a PL protein. PDZ and PL proteins are a binding pair given in

XX specification, or a peptide mimetic of the 3 residue PL protein, or a

XX small molecule having similar functional activity as the 3 residue PL

XX protein. The reagents of the invention have the following activities:

XX anti-inflammatory, anti-allergic, anti-cancer, antipsoriatic, antiasthmatic,

XX dermatological, neuroprotective, virucide, antidiabetic, osteopathic,

XX antiarthritic, immunosuppressive, antiatherosclerotic, cytostatic, anti-

XX HIV, vasotropic, and immunomodulator. The novel modulator is useful for

XX treating a disease correlated with binding between a PDZ protein and PL

XX protein. The disease can be a neurological disease, immune response

XX disease, muscular disease or cancer. The modulator is useful for

XX modulating vesicular trafficking, tumour suppression, signal

XX transduction, protein sorting, establishment of membrane polarity,

XX apoptosis, regulation of immune response and organisation of synapse

XX formation. The modulator is useful for facilitating the assembly of multi

XX -protein complexes, often serving as a bridge between several proteins,

XX or regulating the function of other proteins, and to inhibit leukocyte

XX activation. The modulator is useful for treating diseases characterised

XX by inflammatory and humoral immune responses e.g., inflammation, allergy,

XX CC inflammatory bowel diseases, ulcerative colitis, psoriasis, asthma,

XX allergic rhinitis, atopic dermatitis, arthritis, multiple sclerosis,

XX diabetes, osteoarthritis, graft-versus-host diseases, atherosclerosis,

XX CC

CC leukaemia, infectious diseases (viral infection such as human
 CC immunodeficiency virus (HIV)), and ischaemia. This sequence represents a
 CC PL protein C-terminal core peptide of a cell adhesion molecule of the
 CC invention.
 XX
 SQ Sequence 5 AA;

Query Match 94.7%; Score 18; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSUF 5
 ||||
 Db 1 SSUF 4

RESULT 6
 AAR10519
 ID AAR10519 standard; protein; 6 AA.

XX AC AAR10519;
 XX
 DT 27-AUG-2003 (revised)
 DT 15-APR-1991 (first entry)

DE Fusinus inhibitory peptide B1.

XX muscular contraction-inhibitory neuro-peptide; FIPB1; Mollusca;
 KW radular tractile muscle.

XX Fusinus ferrugineus.

XX JP02306995-A.

XX 20-DEC-1990.

XX 19-MAY-1989; 89JP-00125596.

XX 19-MAY-1989; 89JP-00125596.

XX (SUNR) SUNTORY LTD.

XX WPI; 1991-040149/06.

XX Muscular contraction-inhibitory neuro-peptide(s) in mollusca - prepd. by
 PT purifying oligopeptide using high power liq. chromatography after
 PT extracting neuro:ganglion of Fusinus perplex ferrugineus.

XX Claim 6; Page 1; 10pp; Japanese.

XX The peptide was isolated from Fusinus perplex ferrugineus neuroganglia
 CC and inhibits muscular contraction, especially of the radular tractile
 CC muscle in F.perplex ferrugineus, Prosobranchia and other Mollusca.
 CC Alternatively, it can be synthesised by solid-phase techniques. One or
 CC both of the Ser residues at positions 1 or 2 may be absent. The peptide
 CC can be used in biological studies for the development of drugs. See also
 CC AAR10516-R10518 and AAR10520. (Updated on 27-AUG-2003 to correct OS
 CC field.)

XX Sequence 6 AA;

Query Match 94.7%; Score 18; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSUF 5
 ||||
 Db 1 SSUF 4

RESULT 7
 AAW25555
 ID AAW25555 standard; peptide; 6 AA.

XX

AC AAW25555;

DT 25-MAR-2003 (revised)

DT 10-NOV-1997 (first entry)

XX Synthetic ferritin peptide #28.

XX Functional surrogate; analyte; affinity receptor; immunoreactive group;
 KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
 KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
 KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
 KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
 KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
 KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
 KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
 KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.

XX Synthetic.

XX WO9641172-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010498.

XX 07-JUN-1995; 95US-00476375.

XX (CYTO-) CYTOGEN CORP.

XX Lee-Owen FV, Carter JM;

XX WPI; 1997-077284/07.

XX Labelled functional surrogate of an analyte - useful as competitor
 PT molecule in affinity assays, esp. for detecting large macromolecules such
 PT as ferritin.

XX Claim 51; Page 27; 156pp; English.

XX This sequence represents a synthetic ferritin peptide which was used as a
 CC functional surrogate in the conjugate of the invention. The novel
 CC labelled conjugate comprises at least one label attached to a functional
 CC surrogate of an analyte of interest. The surrogate is capable of
 CC competing effectively with the analyte for a limiting amount of an
 CC affinity receptor for the analyte. The conjugate exhibits an activity
 CC that is altered upon interaction with the amount of the analyte present
 CC in a sample. Functional surrogates such as this have an immunoreactive
 CC group that allows the surrogate to compete effectively and with the
 CC analyte for a limiting amount of its affinity receptor. Functional
 CC surrogates are able to mimic naturally occurring analytes. They can be
 CC labelled for use in standard competitive affinity assays (esp. homogenous
 CC immunoassays) for detecting large macromolecules such as polypeptides,
 CC polysaccharides, polynucleotides, glycoproteins and lipid-containing
 CC macromolecules, as well as small haptens. Typical diagnostic analytes for
 CC detection include cardiac or tumour markers, allergens, hormones related
 CC to fertility-pregnancy or analytes associated with infectious disease. In
 CC particular, the assays are useful for detecting ferritin, follicle
 CC stimulating hormone, human growth hormone, immunoglobulin E, prolactin,
 CC parathyroid hormone, human placental lactogen, hepatitis antigens or
 CC antibodies against them, human chorionic gonadotropin, human luteinising
 CC hormone, cytomegalovirus, Chlamydia, Streptococcus A, rubella,
 CC toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin,
 CC carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen
 CC and CA125 (a tumour marker). (Updated on 25-MAR-2003 to correct PI
 CC field.)

XX Sequence 6 AA;

Query Match 94.7%; Score 18; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSIF 5
|||||
Db 2 SSIF 5

RESULT 8

AAW10783
ID AAW10783 standard; peptide; 6 AA.
XX
XX
AC AAW10783;
XX
XX 25-MAR-2003 (revised)
DT 10-NOV-1997 (first entry)
XX

Ferritin motif #26 important for selective binding affinity.

XX Functional surrogate; analyte; affinity receptor; immunoreactive group;
KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.

XX Synthetic.

XX WO9641172-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010498.

XX 07-JUN-1995; 95US-00476375.

XX (CYTO-) CYTOGEN CORP.

XX Lee-Owen FV, Carter JM;

XX WPI; 1997-077284/07.

XX Labelled functional surrogate of an analyte - useful as competitor
PT molecule in affinity assays, esp. for detecting large macromolecules such
PT as ferritin.

XX Claim 51; Page 56; 156pp; English.

XX This sequence represents a peptide motif derived from ferritin which is
CC important for selective binding affinity. Peptides containing motifs such
CC as this may be used as functional surrogates in the conjugate of the
CC invention. The novel labelled conjugate comprises at least one label
CC attached to a functional surrogate of an analyte of interest. The
CC surrogate is capable of competing effectively with the analyte for a
CC limiting amount of an affinity receptor for the analyte. The conjugate
CC exhibits an activity that is altered upon interaction with the amount of
CC receptor and this activity can be measured and related to the amount of
CC the analyte present in a sample. Functional surrogates such as this have
CC an immunoreactive group that allows the surrogate to compete effectively
CC and with the analyte for a limiting amount of its affinity receptor.
CC Functional surrogates are able to mimic naturally occurring analytes.
CC They can be labelled for use in standard competitive affinity assays
CC (esp. homogenous immunoassays) for detecting large macromolecules such as
CC polypeptides, polysaccharides, polynucleotides, glycoproteins and lipid-
CC containing macromolecules, as well as small haptens. Typical diagnostic
CC analytes for detection include cardiac or tumour markers, allergens,
CC hormones related to fertility-pregnancy or analytes associated with
CC infectious disease. In particular, the assays are useful for detecting
CC ferritin, follicle stimulating hormone, human growth hormone,
CC immunoglobulin E, prolactin, parathyroid hormone, human placental
CC lactogen, hepatitis antigens or antibodies against them, human chorionic
CC gonadotropin, human luteinising hormone, cytomegalovirus, Chlamydia,

CC Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin,
CC myosin light chain, troponin, carcinoembryonic antigen, alpha-
CC fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 6 AA;

Query Match 94.7%; Score 18; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSIF 5
|||||
Db 3 SSIF 6

RESULT 9

AAW25549
ID AAW25549 standard; peptide; 6 AA.

XX AAW25549;

XX 25-MAR-2003 (revised)

DT 10-NOV-1997 (first entry)

XX Synthetic ferritin peptide #22.

XX Functional surrogate; analyte; affinity receptor; immunoreactive group;
KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.

XX Synthetic.

XX WO9641172-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010498.

XX 07-JUN-1995; 95US-00476375.

XX (CYTO-) CYTOGEN CORP.

XX Lee-Owen FV, Carter JM;

XX WPI; 1997-077284/07.

XX Labelled functional surrogate of an analyte - useful as competitor
PT molecule in affinity assays, esp. for detecting large macromolecules such
PT as ferritin.

XX Claim 51; Page 26; 156pp; English.

XX This sequence represents a synthetic ferritin peptide which was used as a
CC functional surrogate in the conjugate of the invention. The novel
CC labelled conjugate comprises at least one label attached to a functional
CC surrogate of an analyte of interest. The surrogate is capable of
CC competing effectively with the analyte for a limiting amount of an
CC affinity receptor for the analyte. The conjugate exhibits an activity
CC that is altered upon interaction with the affinity receptor and this
CC activity can be measured and related to the amount of the analyte present
CC in a sample. Functional surrogates such as this have an immunoreactive
CC group that allows the surrogate to compete effectively and with the
CC analyte for a limiting amount of its affinity receptor. Functional
CC surrogates are able to mimic naturally occurring analytes. They can be
CC labelled for use in standard competitive affinity assays (esp. homogenous
CC immunoassays) for detecting large macromolecules such as polypeptides,

CC polysaccharides, polynucleotides, glycoproteins and lipid-containing
 CC macromolecules, as well as small haptens. Typical diagnostic analytes for
 CC detection include cardiac or tumour markers, allergens, hormones related
 CC to fertility-pregnancy or analytes associated with infectious disease. In
 CC particular, the assays are useful for detecting ferritin, follicle
 CC stimulating hormone, human growth hormone, immunoglobulin E, prolactin,
 CC parathyroid hormone, human placental lactogen, hepatitis antigens or
 CC antibodies against them, human chorionic gonadotropin, human luteinising
 CC hormone, cytomegalovirus, Chlamydia, Streptococcus a, rubella,
 CC toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin,
 CC carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen
 CC and CA125 (a tumour marker). (Updated on 25-MAR-2003 to correct PI
 CC field.)
 CC SQ Sequence 6 AA;
 Query Match 94.7%; Score 18; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSLF 5
 Db 1 SSLF 4
 RESULT 10
 AAW25550
 ID AAW25550 standard; peptide; 6 AA.
 XX
 AC AAW25550;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-NOV-1997 (first entry)
 XX
 DE Synthetic ferritin peptide #23.
 XX
 KW Functional surrogate; analyte; affinity receptor; immunoreactive group;
 KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
 KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
 KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
 KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
 KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
 KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
 KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
 KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Biotinylated Glu"
 XX
 FN WO9641172-A1.
 XX
 XX 19-DEC-1996.
 XX
 PD 07-JUN-1996; 96WO-US010498.
 XX
 PF 07-JUN-1995; 95US-00476375.
 XX
 PR (CYTO-) CYTOGEN CORP.
 XX
 XX Lee-Owen FV, Carter JW;
 XX WPI; 1997-077284/07.
 XX
 DR Labelled functional surrogate of an analyte - useful as competitor
 PT molecule in affinity assays, esp. for detecting large macromolecules such
 PT as ferritin.
 XX
 PS Claim 51; Page 26; 156pp; English.
 XX
 CC This sequence represents a synthetic ferritin peptide which was used as a

CC functional surrogate in the conjugate of the invention. The novel
 CC labelled conjugate comprises at least one label attached to a functional
 CC surrogate of an analyte of interest. The surrogate is capable of
 CC competing effectively with the analyte for a limiting amount of an
 CC affinity receptor for the analyte. The conjugate exhibits an activity
 CC that is altered upon interaction with the affinity receptor and this
 CC activity can be measured and related to the amount of the analyte present
 CC in a sample. Functional surrogates such as this have an immunoreactive
 CC group that allows the surrogate to compete effectively and with the
 CC analyte for a limiting amount of its affinity receptor. Functional
 CC surrogates are able to mimic naturally occurring analytes. They can be
 CC labelled for use in standard competitive affinity assays (esp. homogenous
 CC immunoassays) for detecting large macromolecules such as polypeptides,
 CC polysaccharides, polynucleotides, glycoproteins and lipid-containing
 CC macromolecules, as well as small haptens. Typical diagnostic analytes for
 CC detection include cardiac or tumour markers, allergens, hormones related
 CC to fertility-pregnancy or analytes associated with infectious disease. In
 CC particular, the assays are useful for detecting ferritin, follicle
 CC stimulating hormone, human growth hormone, immunoglobulin E, prolactin,
 CC parathyroid hormone, human placental lactogen, hepatitis antigens or
 CC antibodies against them, human chorionic gonadotropin, human luteinising
 CC hormone, cytomegalovirus, Chlamydia, Streptococcus a, rubella,
 CC toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin,
 CC carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen
 CC and CA125 (a tumour marker). (Updated on 25-MAR-2003 to correct PI
 CC field.)
 CC SQ Sequence 6 AA;
 Query Match 94.7%; Score 18; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSLF 5
 Db 1 SSLF 4
 RESULT 11
 ADD11975
 ID ADD11975 standard; peptide; 6 AA.
 XX
 AC ADD11975;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Cell adhesion molecule PL protein C-terminal core peptide #278.
 XX
 KW modulator; PDZ; post-synaptic density protein 95; PSD95;
 KW Drosophila large disc protein; Zonula Occludin 1 protein; ZO-1;
 KW PDZ ligand; PL; antiinflammatory; antiallergic; antitumor; antipsoriatic;
 KW antischmatic; dermatological; neuroprotective; virucide; antidiabetic;
 KW osteopathic; anti-HIV; vasotropic; immunosuppressive; antiatherosclerotic;
 KW immune response disease; muscular disease; cancer;
 KW modulating vesicular trafficking; tumour suppression;
 KW signal transduction; protein sorting; membrane polarity; apoptosis;
 KW synapse formation; multi-protein complex; leukocyte activation inhibitor;
 KW cell adhesion molecule.
 XX
 OS Unidentified.
 XX
 PN WO2003014303-A2.
 XX
 XX 20-FEB-2003.
 PD
 XX
 PF 02-AUG-2002; 2002WO-US024555.
 XX
 PR 03-AUG-2001; 2001US-0309841P.
 PR 25-FEB-2002; 2002US-0360061P.
 XX
 PA (ARBO-) ARBOR VITA CORP.

PI Lu PS, Rabinowitz JD, Schweizer J, Carrick DM;
 XX WPI; 2003-268193/26.
 XX
 PT Modulator of binding between discs-large homology repeat protein, PDZ and
 PT PDZ ligand protein, is a peptide having few residues of C-terminal
 PT sequence of PDZ ligand protein.
 XX
 XX Disclosure; Page 35; 172pp; English.
 PS
 XX The invention relates to a novel modulator of binding between a PDZ
 CC protein (post-synaptic density protein 95 (PSD95), Drosophila large disc
 CC protein and Zonula Occludin 1 protein (ZO-1)) and a PDZ ligand (PL)
 CC protein. The modulator is a peptide having 3 residues of a C-terminal
 CC sequence of a PL protein. PDZ and PL proteins are a binding pair given in
 CC specification, or a peptide mimetic of the 3 residue PL protein, or a
 CC small molecule having similar functional activity as the 3 residue PL
 CC protein. The reagents of the invention have the following activities:
 CC anti-inflammatory, antiallergic, antitumor, antiparasitic, antiasthmatic,
 CC dermatological, neuroprotective, virucide, antidiabetic, osteopathic,
 CC antiarthritic, immunosuppressive, antiatherosclerotic, cytostatic, anti-
 CC HIV, vasotropic, and immunomodulator. The novel modulator is useful for
 CC treating a disease correlated with binding between a PDZ protein and PL
 CC protein. The disease can be a neurological disease, immune response
 CC disease, muscular disease or cancer. The modulator is useful for
 CC modulating vesicular trafficking, tumour suppression, signal
 CC transduction, protein sorting, establishment of membrane polarity,
 CC apoptosis, regulation of immune response and organisation of synapse
 CC formation. The modulator is useful for facilitating the assembly of multi-
 CC protein complexes often serving as a bridge between several proteins,
 CC or regulating the function of other proteins, and to inhibit leukocyte
 CC activation. The modulator is useful for treating diseases characterised
 CC by inflammatory and humoral immune responses e.g., inflammation, allergy,
 CC inflammatory bowel diseases, ulcerative colitis, psoriasis, asthma,
 CC allergic rhinitis, atopic dermatitis, arthritis, multiple sclerosis,
 CC diabetes, osteoarthritis, graft-versus-host diseases, atherosclerosis,
 CC leukaemia, infectious diseases (viral infection such as human
 CC immunodeficiency virus (HIV)), and ischaemia. This sequence represents a
 CC PL protein C-terminal core peptide of a cell adhesion molecule of the
 XX invention.
 XX
 SQ Sequence 6 AA;
 Query Match 94.7%; Score 18; DB 7; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSUF 5
 Db ||||
 2 SSUF 5
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 AAW10802
 ID AAW10802 standard; peptide; 7 AA.
 XX
 XX AAW10802;
 XX
 XX 25-MAR-2003 (revised)
 DT 10-NOV-1997 (first entry)
 XX
 XX Ferritin motif #45 important for selective binding affinity.
 DE
 XX Functional surrogate; analyte; affinity receptor; immunoreactive group;
 KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
 KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
 KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
 KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
 KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
 KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
 KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
 KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
 XX
 OS Synthetic.
 XX WO9641172-A1.
 XX
 XX 19-DEC-1996.
 PD
 XX 07-JUN-1996; 96WO-US010498.
 PF
 XX 07-JUN-1995; 95US-00476375.
 PR
 XX (CYTO-) CYTOGEN CORP.
 PA
 XX Lee-Owen FV, Carter JM;
 PI
 XX WPI; 1997-077284/07.
 DR
 XX Labelled functional surrogate of an analyte - useful as competitor
 PT molecule in affinity assays, esp. for detecting large macromolecules such
 PT as ferritin.
 XX
 XX Claim 56; Page 56; 156pp; English.
 PS
 XX This sequence represents a peptide motif derived from ferritin which is
 CC important for selective binding affinity. Peptides containing motifs such
 CC as this may be used as functional surrogates in the conjugate of the
 CC invention. The novel labelled conjugate comprises at least one label
 CC attached to a functional surrogate of an analyte of interest. The
 CC surrogate is capable of competing effectively with the analyte for a
 CC limiting amount of an affinity receptor for the analyte. The conjugate
 CC exhibits an activity that is altered upon interaction with the affinity
 CC receptor and this activity can be measured and related to the amount of
 CC the analyte present in a sample. Functional surrogates such as this have
 CC an immunoreactive group that allows the surrogate to compete effectively
 CC and with the analyte for a limiting amount of its affinity receptor.
 CC Functional surrogates are able to mimic naturally occurring analytes.
 CC They can be labelled for use in standard competitive affinity assays
 CC (esp. homogenous immunoassays) for detecting large macromolecules such as
 CC polypeptides, polysaccharides, polynucleotides, glycoproteins and lipid-
 CC containing macromolecules, as well as small haptens. Typical diagnostic
 CC analytes for detection include cardiac or tumour markers, allergens,
 CC hormones related to fertility-pregnancy or analytes associated with
 CC infectious disease. In particular, the assays are useful for detecting
 CC ferritin, follicle stimulating hormone, human growth hormone,
 CC immunoglobulin E, prolactin, parathyroid hormone, human placental
 CC lactogen, hepatitis antigens or antibodies against them, human chorionic
 CC gonadotropin, human luteinising hormone, cytomegalovirus, Chlamydia,
 CC Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin,
 CC myosin light chain, troponin, carcinoembryonic antigen, alpha-
 CC fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 7 AA;
 Query Match 94.7%; Score 18; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSUF 5
 Db ||||
 3 SSUF 6
 RESULT 13
 AAW10801
 ID AAW10801 standard; peptide; 7 AA.
 XX
 XX AAW10801;
 XX
 XX 25-MAR-2003 (revised)
 DT 10-NOV-1997 (first entry)
 XX
 XX Ferritin motif #44 important for selective binding affinity.
 DE
 XX

KW Functional surrogate; analyte; affinity receptor; immunoreactive group;
 KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
 KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
 KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
 KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
 KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
 KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
 KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
 KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
 XX
 OS Synthetic.
 XX
 FN WO9641172-A1.
 XX
 XX 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US010498.
 XX
 PR 07-JUN-1995; 95US-00476375.
 XX
 PA (CYTO-) CYTOGEN CORP.
 XX
 PI Lee-Owen FV, Carter JM;
 XX
 DR WPI; 1997-077284/07.
 XX
 PT Labelled functional surrogate of an analyte - useful as competitor
 PT molecule in affinity assays, esp. for detecting large macromolecules such
 PT as ferritin.
 XX
 PS Claim 56; Page 56; 156pp; English.
 XX
 CC This sequence represents a peptide motif derived from ferritin which is
 CC important for selective binding affinity. Peptides containing motifs such
 CC as this may be used as functional surrogates in the conjugate of the
 CC invention. The novel labelled conjugate comprises at least one label
 CC attached to a functional surrogate of an analyte of interest. The
 CC surrogate is capable of competing effectively with the analyte for a
 CC limiting amount of an affinity receptor for the analyte. The conjugate
 CC exhibits an activity that is altered upon interaction with the amount of
 CC receptor and this activity can be measured and related to the amount of
 CC an immunoreactive group that allows the surrogate to compete effectively
 CC and with the analyte for a limiting amount of its affinity receptor.
 CC Functional surrogates are able to mimic naturally occurring analytes.
 CC They can be labelled for use in standard competitive affinity assays
 CC (esp. homogenous immunoassays) for detecting large macromolecules such as
 CC polypeptides, polysaccharides, polynucleotides, glycoproteins and lipid-
 CC containing macromolecules, as well as small haptens. Typical diagnostic
 CC analytes for detection include cardiac or tumour markers, allergens,
 CC hormones related to fertility-pregnancy or analytes associated with
 CC infectious disease. In particular, the assays are useful for detecting
 CC ferritin, follicle stimulating hormone, human growth hormone,
 CC immunoglobulin E, prolactin, parathyroid hormone, human placental
 CC lactogen, hepatitis antigens or antibodies against them, human chorionic
 CC gonadotropin, human luteinising hormone, cytomegalovirus, Chlamydia,
 CC Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin,
 CC myosin light chain, troponin, carcinoembryonic antigen, alpha-
 CC fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 7 AA;

Query Match 94.7%; Score 18; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSUF 5

Db 3 SSUF 6

RESULT 14

AAW10784
 ID AAW10784 standard; peptide; 7 AA.
 XX
 AC AAW10784;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-NOV-1997 (first entry)
 XX
 DE Ferritin motif #27 important for selective binding affinity.
 XX
 KW Functional surrogate; analyte; affinity receptor; immunoreactive group;
 KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
 KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
 KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
 KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
 KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
 KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
 KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
 KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
 XX
 OS Synthetic.
 XX
 PN WO9641172-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US010498.
 XX
 PR 07-JUN-1995; 95US-00476375.
 XX
 PA (CYTO-) CYTOGEN CORP.
 XX
 PI Lee-Owen FV, Carter JM;
 XX
 DR WPI; 1997-077284/07.
 XX
 PT Labelled functional surrogate of an analyte - useful as competitor
 PT molecule in affinity assays, esp. for detecting large macromolecules such
 PT as ferritin.
 XX
 PS Claim 51; Page 56; 156pp; English.
 XX
 CC This sequence represents a peptide motif derived from ferritin which is
 CC important for selective binding affinity. Peptides containing motifs such
 CC as this may be used as functional surrogates in the conjugate of the
 CC invention. The novel labelled conjugate comprises at least one label
 CC attached to a functional surrogate of an analyte of interest. The
 CC surrogate is capable of competing effectively with the analyte for a
 CC limiting amount of an affinity receptor for the analyte. The conjugate
 CC exhibits an activity that is altered upon interaction with the amount of
 CC receptor and this activity can be measured and related to the amount of
 CC an immunoreactive group that allows the surrogate to compete effectively
 CC and with the analyte for a limiting amount of its affinity receptor.
 CC Functional surrogates are able to mimic naturally occurring analytes.
 CC They can be labelled for use in standard competitive affinity assays
 CC (esp. homogenous immunoassays) for detecting large macromolecules such as
 CC polypeptides, polysaccharides, polynucleotides, glycoproteins and lipid-
 CC containing macromolecules, as well as small haptens. Typical diagnostic
 CC analytes for detection include cardiac or tumour markers, allergens,
 CC hormones related to fertility-pregnancy or analytes associated with
 CC infectious disease. In particular, the assays are useful for detecting
 CC ferritin, follicle stimulating hormone, human growth hormone,
 CC immunoglobulin E, prolactin, parathyroid hormone, human placental
 CC lactogen, hepatitis antigens or antibodies against them, human chorionic
 CC gonadotropin, human luteinising hormone, cytomegalovirus, Chlamydia,
 CC Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin,
 CC myosin light chain, troponin, carcinoembryonic antigen, alpha-
 CC fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 7 AA;

Query Match 94.7%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 SSLF 5
Db 3 SSLF 6

RESULT 15

AAW10779
ID AAW10779 standard; peptide; 7 AA.

AC AAW10779;

DT 25-MAR-2003 (revised)

DT 10-NOV-1997 (first entry)

XX Ferritin motif #22 important for selective binding affinity.

XX Functional surrogate; analyte; affinity receptor; immunoreactive group;
KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.

XX Synthetic.

XX WO9641172-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010498.

XX 07-JUN-1995; 95US-00476375.

XX (CYTO-) CYTOGEN CORP.

XX Lee-Owen FV, Carter JW;

XX WPI; 1997-077284/07.

XX Labelled functional surrogate of an analyte - useful as competitor
PT molecule in affinity assays, esp. for detecting large macromolecules such
PT as ferritin.

XX Claim 56; Page 56; 156pp; English.

XX This sequence represents a peptide motif derived from ferritin which is
CC important for selective binding affinity. Peptides containing motifs such
CC as this may be used as functional surrogates in the conjugate of the
CC invention. The novel labelled conjugate comprises at least one label
CC attached to a functional surrogate of an analyte of interest. The
CC surrogate is capable of competing effectively with the analyte for a
CC limiting amount of an affinity receptor for the analyte. The conjugate
CC exhibits an activity that is altered upon interaction with the affinity
CC receptor and this activity can be measured and related to the amount of
CC the analyte present in a sample. Functional surrogates such as this have
CC an immunoreactive group that allows the surrogate to compete effectively
CC and with the analyte for a limiting amount of its affinity receptor.
CC Functional surrogates are able to mimic naturally occurring analytes.
CC They can be labelled for use in standard competitive affinity assays
CC (esp. homogenous immunoassays) for detecting large macromolecules such as
CC polypeptides, polysaccharides, polynucleotides, glycoproteins and lipid-
CC containing macromolecules, as well as small haptens. Typical diagnostic
CC analytes for detection include cardiac or tumour markers, allergens,
CC hormones related to fertility-pregnancy or analytes associated with
CC infectious disease. In particular, the assays are useful for detecting
CC ferritin, follicle stimulating hormone, human growth hormone,

CC immunoglobulin E, prolactin, parathyroid hormone, human placental
CC lactogen, hepatitis antigens or antibodies against them, human chorionic
CC gonadotropin, human luteinising hormone, cytomegalovirus, Chlamydia,
CC Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin,
CC myosin light chain, troponin, carcinoembryonic antigen, alpha-
CC fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 7 AA;

Query Match 94.7%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSLF 5

Db 3 SSLF 6

Search completed: October 26, 2004, 15:59:47
Job time : 24.75 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:54:00 ; Search time 17.5 Seconds
(without alignments)
92.502 Million cell updates/sec

Title: US-10-032-950-8
Perfect score: 19
Sequence: 1 XSLIF 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	94.7	5	13	US-10-032-950-8
2	18	94.7	7	14	US-10-022-066-231
3	18	94.7	9	9	US-09-850-351A-67
4	18	94.7	9	13	US-10-032-950-1
5	18	94.7	9	13	US-10-032-950-2
6	18	94.7	9	13	US-10-032-950-3
7	18	94.7	9	13	US-10-032-950-4
8	18	94.7	9	14	US-10-201-444-3
9	18	94.7	9	14	US-10-022-066-266
10	18	94.7	10	10	US-09-572-270A-470
11	18	94.7	11	14	US-10-097-175-86
12	18	94.7	11	14	US-10-293-086-12
13	18	94.7	12	15	US-10-435-666-1

14	18	94.7	12	16	US-10-706-391-42	Sequence 42, Appl
15	18	94.7	12	16	US-10-706-391-43	Sequence 43, Appl
16	18	94.7	12	16	US-10-668-600-9	Sequence 9, Appl
17	18	94.7	13	14	US-10-174-613-31	Sequence 31, Appl
18	18	94.7	13	14	US-10-300-694A-5	Sequence 5, Appl
19	18	94.7	13	15	US-10-367-580-289	Sequence 289, App
20	18	94.7	13	15	US-10-367-593-289	Sequence 289, App
21	18	94.7	13	15	US-10-367-594-289	Sequence 289, App
22	18	94.7	13	15	US-10-367-584-289	Sequence 289, App
23	18	94.7	13	15	US-10-367-588-289	Sequence 289, App
24	18	94.7	13	15	US-10-367-668-289	Sequence 289, App
25	18	94.7	13	16	US-10-367-674-289	Sequence 289, App
26	18	94.7	14	14	US-10-158-847-59	Sequence 59, Appl
27	18	94.7	14	14	US-10-158-825-59	Sequence 59, Appl
28	18	94.7	14	16	US-10-346-058-6	Sequence 6, Appl
29	18	94.7	14	16	US-10-158-825-59	Sequence 59, Appl
30	18	94.7	15	9	US-09-759-010-10	Sequence 10, Appl
31	18	94.7	15	15	US-10-367-580-288	Sequence 288, App
32	18	94.7	15	15	US-10-367-593-288	Sequence 288, App
33	18	94.7	15	15	US-10-367-594-288	Sequence 288, App
34	18	94.7	15	15	US-10-367-554-288	Sequence 288, App
35	18	94.7	15	15	US-10-367-558-288	Sequence 288, App
36	18	94.7	15	15	US-10-367-588-288	Sequence 288, App
37	18	94.7	15	16	US-10-367-674-288	Sequence 288, App
38	18	94.7	15	16	US-10-416-249-309	Sequence 309, App
39	18	94.7	15	16	US-10-416-249-310	Sequence 310, App
40	18	94.7	15	16	US-10-416-249-311	Sequence 311, App
41	18	94.7	16	14	US-10-062-831-88	Sequence 88, Appl
42	18	94.7	16	14	US-10-225-567A-1613	Sequence 1613, Ap
43	18	94.7	16	14	US-10-062-599-88	Sequence 88, Appl
44	18	94.7	18	9	US-09-864-761-40860	Sequence 40860, A
45	18	94.7	18	10	US-09-866-066-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-10-032-950-8
; Sequence 8, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-8

Query Match 94.7%; Score 18; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;
QY 2 SSIF 5

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Db          2 SSF 5
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RESULT 2
US-10-022-066-231
; Sequence 231, Application US/10022066
; Publication No. US20030165057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: BRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022.066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 231
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-022-066-231

Query Match          94.7%; Score 18; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 SSF 5
Db          4 SSF 7
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RESULT 3
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; Sequence 67, Application US/09850351A
; Patent No. US2002010080A1
; GENERAL INFORMATION:
; APPLICANT: Feitelson, Jerald S.
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stockhoff, Brian A.
; APPLICANT: Schneits, James
; APPLICANT: Loewer, David
; APPLICANT: Dullum, Charles Joseph
; APPLICANT: Muller-Cohn, Judy
; APPLICANT: Stamp, Lisa
; APPLICANT: Morrill, George
; TITLE OF INVENTION: No. US2002010080A1el Pesticidal Toxins and Nucleotide
; Sequences Which Encode these Toxins
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

US-10-032-950-1
; Sequence 1, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-1

Query Match          94.7%; Score 18; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 SSF 5
Db          1 SSF 4
||||
RESULT 4
US-10-032-950-1
; Sequence 1, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A1ick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-1

Query Match          94.7%; Score 18; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 SSF 5
Db          1 SSF 4
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US-09-850-351A-67
; Sequence Description: SEQ ID NO: 67;
; MOLECULE TYPE: Peptide
; STRANDEDNESS: single
; TOPOLOGY: linear
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-850-351A-67
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QY      2 SSLF 5
      ||||
Db      6 SSLF 9

RESULT 5
US-10-032-950-2
; Sequence 2, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453Alick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-23IN
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-2

Query Match      94.7%; Score 18; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SSLF 5
      ||||
Db      6 SSLF 9

RESULT 6
US-10-032-950-3
; Sequence 3, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453Alick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-23IN
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-3

Query Match      94.7%; Score 18; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SSLF 5
      ||||
Db      6 SSLF 9

RESULT 7
US-10-032-950-4
; Sequence 4, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
; APPLICANT: Muir, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453Alick, Richard P.
; APPLICANT: Beavis, Ronald
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-23IN
; CURRENT APPLICATION NUMBER: US/10/032,950
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-4

Query Match      94.7%; Score 18; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SSLF 5
      ||||
Db      6 SSLF 9

RESULT 8
US-10-201-444-3
; Sequence 3, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT APPLICATION NUMBER: US/10/201,444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; OTHER INFORMATION:
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-201-444-3

Query Match      94.7%; Score 18; DB 14; Length 9;
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSUF 5
Db 6 SSUF 9

RESULT 9
US-10-022-066-266
; Sequence 266, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022.066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 266
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-022-066-266

Query Match 94.7%; Score 18; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSUF 5
Db 6 SSUF 9

RESULT 10
US-09-572-270A-470
; Sequence 470, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 470
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in Unknown at 10-19 and may interact with
US-09-572-270A-470

Query Match 94.7%; Score 18; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSUF 5
Db 6 SSUF 9

Db 7 SSUF 10

RESULT 11
US-10-097-175-86
; Sequence 86, Application US/10097175
; Publication No. US20030045680A1
; GENERAL INFORMATION:
; APPLICANT: JOYAL, JOHN L.
; APPLICANT: MUELLER, JOHN
; APPLICANT: OZA, VIBHA B.
; APPLICANT: FINDEIS, MARK A.
; TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
; FILE REFERENCE: PPI-110
; CURRENT APPLICATION NUMBER: US/10/097,175
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,240
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/352,399
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-86

Query Match 94.7%; Score 18; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSUF 5
Db 2 SSUF 5

RESULT 12
US-10-293-086-12
; Sequence 12, Application US/10293086
; Publication No. US20030134310A1
; GENERAL INFORMATION:
; APPLICANT: Cujec, Thomas P.
; TITLE OF INVENTION: Cellular Kinase Targets and Inhibitors,
; FILE REFERENCE: 50036/048002
; CURRENT APPLICATION NUMBER: US/10/293,086
; CURRENT FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/337,990
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phosphorylation consensus sequence
US-10-293-086-12

Query Match 94.7%; Score 18; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSUF 5
Db 7 SSUF 10

RESULT 13
US-10-435-666-1


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; Sequence 1, Application US/10435666
; Publication No. US20040006001A1
; GENERAL INFORMATION:
; APPLICANT: CARTER, Daniel C.
; TITLE OF INVENTION: FERRITIN FUSION PROTEINS FOR USE IN VACCINES AND OTHER APPLICATIONS
; FILE REFERENCE: P07624W000/BAS
; CURRENT APPLICATION NUMBER: US/10/435,666
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,145
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-435-666-1

Query Match          94.7%; Score 18; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SS LF 5
      |||||
Db      3 SS LF 6

RESULT 14
US-10-706-391-42
; Sequence 42, Application US/10706391
; Publication No. US20040137482A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: WASHINGTON DENTAL SERVICE
; APPLICANT: Eckert, Randal
; APPLICANT: Qi, Fengxia
; APPLICANT: Shi, Wenyuan
; APPLICANT: Anderson, Maxwell H.
; TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
; FILE REFERENCE: 2101363-991600
; CURRENT APPLICATION NUMBER: US/10/706,391
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 10/077,624
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 09/910,358
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide library
US-10-706-391-42

Query Match          94.7%; Score 18; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SS LF 5
      |||||
Db      8 SS LF 11

RESULT 15
US-10-706-391-43
; Sequence 43, Application US/10706391
; Publication No. US20040137482A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

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; APPLICANT: WASHINGTON DENTAL SERVICE
; APPLICANT: Eckert, Randal
; APPLICANT: Qi, Fengxia
; APPLICANT: Shi, Wenyuan
; APPLICANT: Anderson, Maxwell H.
; TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
; FILE REFERENCE: 2101363-991600
; CURRENT APPLICATION NUMBER: US/10/706,391
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 10/077,624
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 09/910,358
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide library
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(12)
; OTHER INFORMATION: Xaa is any amino acid
US-10-706-391-43

Query Match          94.7%; Score 18; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SS LF 5
      |||||
Db      8 SS LF 11

Search completed: October 26, 2004, 16:10:14
Job time : 17.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:46:55 ; Search time 4.85294 Seconds
(without alignments)
99.132 Million cell updates/sec

Title: US-10-032-950-8

Perfect score: 19

Sequence: 1 XSLF 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: Pirl: *
2: Pirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	94.7	18	2 S57518	T cell receptor be
2	18	94.7	20	2 A60739	somatotropin - gui
3	18	94.7	21	2 S03481	T-cell receptor al
4	18	94.7	24	2 PH1697	Ig heavy chain V r
5	18	94.7	24	2 PH1696	Ig heavy chain V r
6	18	94.7	29	2 E47719	house-dust-mite-re
7	18	94.7	34	2 T11814	hypothetical prote
8	18	94.7	45	2 B30821	hypothetical prote
9	18	94.7	47	2 C39925	AgRD protein limpo
10	18	94.7	54	2 S34728	ribose-phosphate d
11	18	94.7	54	2 T06514	hypothetical prote
12	18	94.7	55	2 B71683	hypothetical prote
13	18	94.7	59	2 S01877	NADH2 dehydrogenas
14	18	94.7	62	2 T07470	hypothetical prote
15	18	94.7	62	2 H72168	A43R protein - var
16	18	94.7	65	2 P00719	glutalin II 7.4/32
17	18	94.7	66	2 C82699	hypothetical prote
18	18	94.7	70	2 A84033	hypothetical prote
19	18	94.7	71	2 T18055	hypothetical prote
20	18	94.7	71	2 B82025	hypothetical prote
21	18	94.7	73	2 T25649	hypothetical prote
22	18	94.7	74	2 E82864	plasmid stabilizat
23	18	94.7	75	2 A81539	exodeoxyribonuclea
24	18	94.7	76	2 T17719	hypothetical prote
25	18	94.7	77	2 A86399	protein P17L21.12
26	18	94.7	78	2 T03930	gene GUR15 protein
27	18	94.7	79	2 T02948	hypothetical prote
28	18	94.7	80	2 D33285	ubiquinol-cytochro
29	18	94.7	80	2 C81003	hypothetical prote

30 18 94.7 80 2 S19984 hypothetical prote
31 18 94.7 80 2 S19987 hypothetical prote
32 18 94.7 82 2 C69013 hypothetical prote
33 18 94.7 83 2 C84274 hypothetical prote
34 18 94.7 84 2 A82604 hypothetical prote
35 18 94.7 85 2 C82369 this protein VC006
36 18 94.7 92 1 Q8ECXP hypothetical prote
37 18 94.7 93 2 G84521 hypothetical prote
38 18 94.7 93 2 C71984 hypothetical prote
39 18 94.7 95 2 AG0277 probable phage-rel
40 18 94.7 97 2 A83971 hypothetical prote
41 18 94.7 99 2 F98105 conserved hypobeth
42 18 94.7 100 2 S44892 ZK112.4 protein -
43 18 94.7 101 2 S73700 probable lipoprote
44 18 94.7 101 2 T38892 very hypothetical
45 18 94.7 102 2 G71025 hypothetical prote

ALIGNMENTS

RESULT 1

S57518
T cell receptor beta chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57518
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified;
A;Reference number: S57494
A;Accession: S57518
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-18 <BUR>
A;Cross-references: EMBL:749920; NID:9887490; PIDN:CAA90166.1; PID:9887491
C;Keywords: T-cell receptor

Query Match 94.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSLF 5

DB 3 SSLF 6

RESULT 2

A60739
somatotropin - guinea pig (fragment)
N;Alternate names: growth hormone
C:Species: Cavia porcellus (guinea pig)
C>Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 17-Mar-1999
C:Accession: A60739
R;Gabrielsson, B.; Fairhall, K.M.; Robinson, I.C.A.F.
J. Endocrinol. 124, 371-380, 1990
A;Title: Growth hormone secretion in the guinea-pig.
A;Reference number: A60739; MUID:90237710; PMID:1970601
A;Accession: A60739
A;Molecule type: protein
A;Residues: 1-20 <GNB>
C;Comment: The growth hormone system in the guinea pig is unusual among mammals in that
C;Superfamily: prolactin
C;Keywords: anterior pituitary; growth factor; hormone

Query Match 94.7%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSLF 5

DB 7 SSLF 10

RESULT 3
S03481
T-cell receptor alpha chain J region (TA20) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Nov-1999
C:Accession: S03481
R:Arden, B.; Klotz, J.L.; Siu, G.; Hood, L.E.
Nature 316, 783-787, 1985
A:Title: Diversity and structure of genes of the alpha family of mouse T-cell antigen re
A:Reference number: S03467; MUID:85296324; PMID:3839904
A:Accession: S03481
A:Molecule type: mRNA
A:Residues: 1-21 <ARD>
A:Cross-references: EMBL:X02975; NID:954392; PIDN:CAA6717.1; PID:G773240
C:Note: This sequence was determined from the differentiated gene
C:Keywords: T-cell receptor
F:1-17/Domain: T-cell receptor alpha chain J region #status predicted <JRB>
Query Match 94.7%; Score 18; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 77; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;
QY 2 SSFL 5
DB 2 SSFL 5
RESULT 4
PH1697
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1697; PH1699
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1697
A:Molecule type: mRNA
A:Residues: 1-24 <MCH>
A:Experimental source: B cell; clone NP-7-10
A:Note: the authors translated the codon GCT for residue 23 as Asp
A:Accession: PH1699
A:Molecule type: mRNA
A:Residues: 1-10, 'A', 12-13, 'R', 15-20, 'T', 22, 'D', 24 <MC2>
A:Experimental source: B cell; clone NP-7-12
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
Query Match 94.7%; Score 18; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 89; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;
QY 2 SSFL 5
DB 19 SSFL 22
RESULT 5
PH1696
Ig heavy chain V region (clone NP-7-9) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1696
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1696
A:Molecule type: mRNA
A:Residues: 1-24 <MCH>
A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 94.7%; Score 18; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSFL 5
DB 19 SSFL 22

RESULT 6

E47719
house-dust-mite-reactive T-cell receptor beta chain (CD4+ clone DE26, V(D)J junctional r
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: E47719
R:Wedderburn, L.R.; O'Hehir, R.E.; Hewitt, C.R.; Lamb, J.R.; Owen, M.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 8214-8218, 1993
A:Title: In vivo clonal dominance and limited T-cell receptor usage in human CD4+ T-cell
A:Reference number: A47719; MUID:93376774; PMID:8367485
A:Accession: E47719
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-29 <WED>
A:Note: sequence extracted from NCBI backbone (NCBIN:137825, NCBI:P:137831)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
Query Match 94.7%; Score 18; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSFL 5
DB 3 SSFL 6

RESULT 7

T11814
hypothetical protein ORF34a - Norway spruce chloroplast
C:Species: chloroplast Picea abies (Norway spruce)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T11814
R:Kluemper, S.; Kanka, S.; Riesner, D.; Btscheid, M.
submitted to the EMBL Data Library, March 1997
A:Description: Characterisation of a Norway spruce chloroplast DNA clone: Complete nucle
A:Reference number: Z17349
A:Accession: T11814
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-34 <KLU>
A:Cross-references: UNIPROT:O62958; EMBL:U92462; NID:G2959581; PID:G2959590
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast
Query Match 94.7%; Score 18; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSFL 5
DB 13 SSFL 16

RESULT 8

B90821
hypothetical protein ECS1538 [imported] - Escherichia coli (strain O157:H7, substrain RL
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: B90821

R.; Batuecas, B.; Garesse, R.; Calleja, M.; Valverde, J.R.; Marco, R.
Nucleic Acids Res. 16, 6515-6529, 1988
A:Title: Genome organization of Artemia mitochondrial DNA.
A:Reference number: S01207; MUID:88289417; PMID:3135541
A:Accession: S01877
A:Molecule type: DNA
A:Residues: 1-59 <BAT>
A:Cross-references: EMBL:X07663; NID:9600442; PID:9600443
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC4
C:Keywords: mitochondrion; NAD; oxidoreductase

Query Match 94.7%; Score 18; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSUF 5
Db 30 SSUF 33

RESULT 14

T07470

hypothetical protein 62b - Japanese black pine chloroplast
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07470
R:Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
A:Reference number: Z16030; MUID:95024047; PMID:7937893
A:Accession: T07470
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-62 <WAK>
A:Cross-references: UNIPROT:P52805; EMBL:D17510; NID:g529643; PIDN:BAA04348.1; PID:g1262
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 94.7%; Score 18; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSUF 5
Db 56 SSUF 59

RESULT 15

H72168

A43R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
C:Accession: H72168
R:Shchelkunov, S.N.; Tomenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopan
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: H72168
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <SHC>
A:Cross-references: UNIPROT:Q99183; GB:Y16780; NID:g5830555; PIDN:CAB54746.1; PID:e15427
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: A43R

Query Match 94.7%; Score 18; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSUF 5
Db 5 SSUF 8

Search completed: October 26, 2004, 16:06:13
Job time : 6.85294 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:44:50 ; Search time 22.5735 Seconds
(without alignments)
127.445 Million cell updates/sec

Title: US-10-032-950-8
Perfect score: 19
Sequence: 1 XSLF 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues 1825181
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	94.7	17	2 Q95795	O95795 homo sapien
2	18	94.7	27	2 Q9R7V1	Q9R7V1 staphylococ
3	18	94.7	27	2 Q9Z068	Q9Z068 hepatitis c
4	18	94.7	27	2 Q91JF4	Q91JF4 hepatitis c
5	18	94.7	27	2 Q91JF5	Q91JF5 hepatitis c
6	18	94.7	27	2 Q9J5X4	Q9J5X4 hepatitis c
7	18	94.7	27	2 Q9J5X7	Q9J5X7 hepatitis c
8	18	94.7	27	2 Q9J5X8	Q9J5X8 hepatitis c
9	18	94.7	27	2 Q9J5X9	Q9J5X9 hepatitis c
10	18	94.7	27	2 Q9J5Y0	Q9J5Y0 hepatitis c
11	18	94.7	27	2 Q9J5Y2	Q9J5Y2 hepatitis c
12	18	94.7	27	2 Q9J5Y5	Q9J5Y5 hepatitis c
13	18	94.7	27	2 Q9J5Y6	Q9J5Y6 hepatitis c
14	18	94.7	27	2 Q9QSL9	Q9QSL9 hepatitis c
15	18	94.7	27	2 Q9QSM0	Q9QSM0 hepatitis c
16	18	94.7	27	2 Q9QSM1	Q9QSM1 hepatitis c
17	18	94.7	27	2 Q9QSM2	Q9QSM2 hepatitis c
18	18	94.7	27	2 Q9QSM3	Q9QSM3 hepatitis c
19	18	94.7	27	2 Q9QSM4	Q9QSM4 hepatitis c
20	18	94.7	27	2 Q9QSM5	Q9QSM5 hepatitis c
21	18	94.7	27	2 Q9QSM6	Q9QSM6 hepatitis c
22	18	94.7	27	2 Q9QSM7	Q9QSM7 hepatitis c
23	18	94.7	27	2 Q9QSM8	Q9QSM8 hepatitis c
24	18	94.7	27	2 Q9QSP4	Q9QSP4 hepatitis c
25	18	94.7	27	2 Q9QSP5	Q9QSP5 hepatitis c
26	18	94.7	27	2 Q9QSP7	Q9QSP7 hepatitis c
27	18	94.7	32	2 Q72829	Q72829 desulfovibr
28	18	94.7	32	2 AAS96925	AAS96925 desulfovi
29	18	94.7	35	2 Q62958	Q62958 picea abies
30	18	94.7	35	2 Q9GS04	Q9GS04 arabidopsis
31	18	94.7	35	2 Q9JM75	Q9JM75 mus musculu

32 18 94.7 35 2 O9QOT0
33 18 94.7 36 2 Q94RP7
34 18 94.7 36 2 Q9VTR8
35 18 94.7 36 2 Q9VTS0
36 18 94.7 36 2 Q9VTS5
37 18 94.7 36 2 Q9VTS7
38 18 94.7 37 2 Q7QUO8
39 18 94.7 38 1 PSBI_CNAME
40 18 94.7 38 2 Q87K38
41 18 94.7 39 2 Q8TGU9
42 18 94.7 40 2 Q9TR19
43 18 94.7 40 2 Q91K09
44 18 94.7 40 2 Q91K70
45 18 94.7 41 2 Q8IR66

ALIGNMENTS

RESULT 1

O95795 PRELIMINARY; PRT; 17 AA.
AC O95795;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Advanced glycosylation end product-specific receptor (Fragment).
GN Name=RAGE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Blazkova M., Kankova K.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF065211; AAL5888.1; -;
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1727 MW; 38C7EE8959E0D72 CRC64;

Query Match 94.7%; Score 18; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSIF 5
Db 9 SSIF 12

RESULT 2

O9R7V1 PRELIMINARY; PRT; 27 AA.
AC O9R7V1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutamic acid-specific protease (EC 3.4.21.19) (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93152142; PubMed=1369143;
RX STRAIN=ATCC12260;
RA "Kakudo S., Yoshikawa K., Tamaki M., Nakamura E., Teraoka H.;
RT "Secretory expression of a glutamic-acid-specific endopeptidase
RT (Spase) from Staphylococcus aureus ATCC12600 in Bacillus subtilis.";
RL Appl. Microbiol. Biotechnol. 38:226-233(1992).
DR EMBL; D10369; BAA1899.1; -;
DR GO; GO:0008233; F:peptidase activity; IEA.

KW Hydrolase; Protease.
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2769 MW; 707B66F95EC388D4 CRC64;
 Query Match 94.7%; Score 18; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSUF 5
 Db 9 SSUF 12

RESULT 3
 ID Q92068 PRELIMINARY; PRT; 27 AA.
 AC Q92068;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE E2 region (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98411405; PubMed=9738045;
 RA Mizuno M., Higuchi T., Kamatsuse K., Esumi M.;
 RT "Genetic and serological evidence for multiple instances of
 RT unrecognized transmission of hepatitis C virus in hemodialysis
 RT units";
 RL J. Clin. Microbiol. 36:2926-2931(1998).
 DR EMBL; AB001404; BAA35043.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR002531; HCV NS1.
 DR Pfam; PF01560; HCV NS1.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2749 MW; AB46C291E9E2F4A4 CRC64;
 Query Match 94.7%; Score 18; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSUF 5
 Db 17 SSUF 20

RESULT 4
 ID Q91JF4 PRELIMINARY; PRT; 27 AA.
 AC Q91JF4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Envelope protein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Alberto S.-F.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF221141; AAF7703.1; -.
 DR GO; GO:0019031; C: viral envelope; IEA.

KW Envelope protein.
 FT NON_TER 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2716 MW; C8F6555E3CF5925A CRC64;
 Query Match 94.7%; Score 18; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSUF 5
 Db 16 SSUF 19

RESULT 5
 ID Q91JF5 PRELIMINARY; PRT; 27 AA.
 AC Q91JF5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope protein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Alberto S.-F.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF221140; AAF7702.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR002531; HCV NS1.
 DR Pfam; PF01560; HCV NS1.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2715 MW; C8F6555E3CF59763 CRC64;
 Query Match 94.7%; Score 18; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SSUF 5
 Db 16 SSUF 19

RESULT 6
 ID Q9J5X4 PRELIMINARY; PRT; 27 AA.
 AC Q9J5X4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20219428; PubMed=10756048;
 RA Manzini A., Solfrosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
 RA Zanetti A.R., Clementi M.;
 RT "Dominant role of host selective pressure in driving hepatitis C virus
 RT evolution in perinatal infection";
 RL J. Virol. 74:4327-4334(2000).
 DR EMBL; AF192435; AAF65646.1; -.

KW Polyprotein. 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2839 MW; 2C7284EC79B20A04 CRC64;
 Query Match 94.7%; Score 18; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSUF 5
 Db 17 SSUF 20

RESULT 7
 Q9J5X7 PRELIMINARY; PRT; 27 AA.
 ID Q9J5X7
 AC Q9J5X7;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
 DE Polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20219428; PubMed=10756048;
 RA Manzin A., Solforosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
 RA Zanetti A.R., Clementi M.;
 RT "Dominant role of host selective pressure in driving hepatitis C virus
 evolution in perinatal infection.";
 RL J. Virol. 74:4327-4334(2000).
 DR EMBL; AF192432; AAF65643.1; -.
 KW Polyprotein. 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2842 MW; 2C72814C79B20A04 CRC64;
 Query Match 94.7%; Score 18; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSUF 5
 Db 17 SSUF 20

RESULT 8
 Q9J5X8 PRELIMINARY; PRT; 27 AA.
 ID Q9J5X8
 AC Q9J5X8;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
 DE Polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20219428; PubMed=10756048;
 RA Manzin A., Solforosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
 RA Zanetti A.R., Clementi M.;
 RT "Dominant role of host selective pressure in driving hepatitis C virus
 evolution in perinatal infection.";
 RL J. Virol. 74:4327-4334(2000).
 DR EMBL; AF192431; AAF65642.1; -.
 KW Polyprotein. 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2856 MW; 8C22814C79B20A02 CRC64;
 Query Match 94.7%; Score 18; DB 2; Length 27;

SQ SEQUENCE 27 AA; 2825 MW; 2C72839C79B20A04 CRC64;
 Query Match 94.7%; Score 18; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSUF 5
 Db 17 SSUF 20

RESULT 9
 Q9J5X9 PRELIMINARY; PRT; 27 AA.
 ID Q9J5X9
 AC Q9J5X9;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
 DE Polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20219428; PubMed=10756048;
 RA Manzin A., Solforosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
 RA Zanetti A.R., Clementi M.;
 RT "Dominant role of host selective pressure in driving hepatitis C virus
 evolution in perinatal infection.";
 RL J. Virol. 74:4327-4334(2000).
 DR EMBL; AF192430; AAF65641.1; -.
 KW Polyprotein. 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2841 MW; 164299FB29B20A1E CRC64;
 Query Match 94.7%; Score 18; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSUF 5
 Db 17 SSUF 20

RESULT 10
 Q9J5Y0 PRELIMINARY; PRT; 27 AA.
 ID Q9J5Y0
 AC Q9J5Y0;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
 DE Polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20219428; PubMed=10756048;
 RA Manzin A., Solforosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
 RA Zanetti A.R., Clementi M.;
 RT "Dominant role of host selective pressure in driving hepatitis C virus
 evolution in perinatal infection.";
 RL J. Virol. 74:4327-4334(2000).
 DR EMBL; AF192429; AAF65640.1; -.
 KW Polyprotein. 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2856 MW; 8C22814C79B20A02 CRC64;
 Query Match 94.7%; Score 18; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSUF 5
Db 17 SSUF 20

RESULT 11
Q9J5Y2 PRELIMINARY; PRT; 27 AA.
ID Q9J5Y2
AC Q9J5Y2
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE Polypeptide (Fragment)
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219428; PubMed=10756048;
RA Manzini A., Solfrosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
RA Zanetti A.R., Clementi M.;
RT "Dominant role of host selective pressure in driving hepatitis C virus
evolution in perinatal infection.";
RL J. Virol. 74:4327-4334(2000).
DR EMBL; AF192427; AAF65638.1; -.
KW Polypeptide.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2839 MW; 2C72910C79B20A04 CRC64;

Query Match 94.7%; Score 18; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSUF 5
Db 17 SSUF 20

RESULT 12
Q9J5Y5 PRELIMINARY; PRT; 27 AA.
ID Q9J5Y5
AC Q9J5Y5
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE Polypeptide (Fragment)
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219428; PubMed=10756048;
RA Manzini A., Solfrosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
RA Zanetti A.R., Clementi M.;
RT "Dominant role of host selective pressure in driving hepatitis C virus
evolution in perinatal infection.";
RL J. Virol. 74:4327-4334(2000).
DR EMBL; AF192424; AAF65635.1; -.
KW Polypeptide.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2852 MW; 08B36BEC79B20A1E CRC64;

Query Match 94.7%; Score 18; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSUF 5
Db 17 SSUF 20

RESULT 13
Q9J5Y6 PRELIMINARY; PRT; 27 AA.
ID Q9J5Y6
AC Q9J5Y6
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE Polypeptide (Fragment)
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219428; PubMed=10756048;
RA Manzini A., Solfrosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
RA Zanetti A.R., Clementi M.;
RT "Dominant role of host selective pressure in driving hepatitis C virus
evolution in perinatal infection.";
RL J. Virol. 74:4327-4334(2000).
DR EMBL; AF192423; AAF65634.1; -.
KW Polypeptide.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2866 MW; 164284EC79B20A1E CRC64;

Query Match 94.7%; Score 18; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSUF 5
Db 17 SSUF 20

RESULT 14
Q8QSL9 PRELIMINARY; PRT; 27 AA.
ID Q8QSL9
AC Q8QSL9
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE E2 protein (Fragment)
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22786443; PubMed=12904364;
RA Gaudy C., Moreau A., Veillon P., Temoin S., Lunel F., Goudeau A.;
RT "Significance of pretreatment analysis of hepatitis C virus genotype
1b hypervariable region 1 sequences to predict antiviral outcome.";
RL J. Clin. Microbiol. 41:3615-3622(2003).
DR EMBL; AF473776; AAL86846.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2704 MW; A7EF16444073C4D5 CRC64;

Query Match 94.7%; Score 18; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSUF 5
Db 17 SSUF 20

Best Local Similarity 100.0%; Pred. No. 9.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 2 SSUF 5
Db 17 SSUF 20

RESULT 15

Q8QSMC PRELIMINARY; PRT; 27 AA.
AC Q8QSMO
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E2 protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22786443; PubMed=12904364;
RA Gaudy C., Moreau A., Veillon P., Temoin S., Lunel F., Goudeau A.;
RT "Significance of pretreatment analysis of hepatitis C virus genotype
RT 1b hypervariable region 1 sequences to predict antiviral outcome.";
RL J. Clin. Microbiol. 41:3615-3622(2003).
DR EMBL; AF473775; AAU86845.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR02531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI; I.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON TER 1
FT NON TER 1
FT NON TER 27
SQ SEQUENCE 27 AA; 2674 MW; A7F417P44073C4D5 CRC64;

Query Match 94.7%; Score 18; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 9.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 2 SSUF 5
Db 17 SSUF 20

Search completed: October 26, 2004, 16:05:08
Job time : 23.5735 secs

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